GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 3, 2003, 23:04:17 ; Search time 4272.77 Seconds
(without alignments)
17041.707 Million cell updates/sec

Title: US-10-027-000-3
Perfect score: 2502
Sequence: 1 atggctgatattgatgttga.....attggtggtctggcgtgtaa 2502

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
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23: em_pat:*
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26: em_ro:*
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	427	17.1	4193	8	KFBGLUC	X05918 Kluyveromyc
2	406.2	16.2	38269	1	AF486581	AF486581 Unculture
3	393.6	15.7	39305	8	SPU33009	U33009 Schizosacch
4	393.6	15.7	41799	8	SPBC1683	AL355920 Schizosac
5	393.6	15.7	85837	8	SPU33010	U33010 Schizosacch
6	392.2	15.7	2793	8	AF329731	AF329731 Volvariel
7	350.4	14.0	3578	1	AF005277	AF005277 Cellulomo
8	343.4	13.7	3710	1	ATUCBG1	M59852 A.tumefacie
9	302.2	12.1	2636	8	ABI293760	AJ293760 Agaricus
c 10	270	10.8	110000	1	REU80928_2	Continuation (3 of
11	205	8.2	2601	6	AX489445	AX489445 Sequence
12	197.4	7.9	37445	1	SC8A6	AL031013 Streptomy
13	184.4	7.4	3241	6	AR173232	AR173232 Sequence
14	184.4	7.4	17665	1	AF521878	AF521878 Streptomy
c 15	178.2	7.1	2760	1	SEY14327	Y14327 Saccharopol
16	175.2	7.0	12441	1	AF079762	AF079762 Streptomy
17	161	6.4	2256	6	E11369	E11369 DNA encodin
18	157.2	6.3	2640	1	TNBGLB	Z77856 T.neapolita
19	156.8	6.3	3179	1	CEGDGB	D14068 C.gilvus ge
c 20	152.2	6.1	11763	1	AE005774	AE005774 Caulobact
21	149.4	6.0	14878	1	AE005849	AE005849 Caulobact
c 22	143.6	5.7	10615	1	AE012240	AE012240 Xanthomon
c 23	138.6	5.5	15052	1	AF055579	AF055579 Streptomy
c 24	138.6	5.5	50937	6	AR159871	AR159871 Sequence
c 25	137.4	5.5	21243	1	AE001690	AE001690 Thermotog
26	136.2	5.4	3265	1	RAU92808	U92808 Ruminococcu
27	135.8	5.4	2166	6	AR205082	AR205082 Sequence
28	132.6	5.3	3158	1	RALBGLT	X15415 Ruminococcu
c 29	129.2	5.2	2075	1	ARGERMA	M11276 Arthrobacte
30	127.6	5.1	2620	1	CSBGLZ	Z94045 C.stercorar
31	127.6	5.1	4537	1	AF090429	AF090429 Azospiril
32	126.4	5.1	2346	1	PAL276021	AJ276021 Prevotell
c 33	126	5.0	12140	1	AE011777	AE011777 Xanthomon
c 34	123.2	4.9	110000	2	LMFLCHR36_08	Continuation (9 of
35	118.2	4.7	3542	1	AB071166	AB071166 Gluconace
36	117.2	4.7	3955	1	MIBBGLA	L06134 Microbispor
c 37	114.4	4.6	11557	1	AE004598	AE004598 Pseudomon
38	111.6	4.5	15852	1	AE006929	AE006929 Mycobacte
39	111.6	4.5	36300	1	MTCI28	Z97050 Mycobacteri
40	109	4.4	13332	1	AE005788	AE005788 Caulobact
41	106.2	4.2	2370	1	PRU35425	U35425 Prevotella
42	104.4	4.2	2894	1	CTBGLB	X15644 Clostridium
c 43	104.4	4.2	12882	1	AE013715	AE013715 Yersinia
44	104.4	4.2	150754	9	AC023491	AC023491 Homo sapi
45	104.4	4.2	258050	1	AJ414153	AJ414153 Yersinia

ALIGNMENTS

RESULT 1
KFBGLUC
LOCUS KFBGLUC 4193 bp DNA linear PLN 12-SEP-1993
DEFINITION Kluyveromyces fragilis beta-glucosidase gene.
ACCESSION X05918
VERSION X05918.1 GI:2804
KEYWORDS beta-glucosidase.
SOURCE Kluyveromyces marxianus.
ORGANISM Kluyveromyces marxianus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
REFERENCE 1 (bases 1 to 4193)
AUTHORS Raynal,A., Gerbaud,C., Francingues,M.C. and Guerineau,M.
TITLE Sequence and transcription of the beta-glucosidase gene of
Kluyveromyces fragilis cloned in Saccharomyces cerevisiae

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  JOURNAL   Curr. Genet. 12 (3), 175-184 (1987)
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   PUBMED   2835179
FEATURES             Location/Qualifiers
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                     /organism="Kluyveromyces marxianus"
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                     /clone_lib="PHCG3"
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                     GAGTKERTKKLTLKKGQVYNVRVEYGSGPTSGLVGEFGAGGFQAGVIKAIDDDEEIRN
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                     VDVKNTGDKFAGSEVVQVYFSALNSKVSRPVKELKGFEKVHLEPGEKKTVNIELELKD
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     misc_feature    3442. .3445
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     misc_feature    3498. .3501
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     misc_feature    3541. .3543
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     repeat_unit     3642. .3652
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BASE COUNT     1338 a    675 c    941 g   1239 t
ORIGIN

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  Best Local Similarity   50.7%;  Pred. No. 1.5e-42;
  Matches 1253;  Conservative    0;  Mismatches 1155;  Indels   63;  Gaps    7;

Qy      1 ATGGCTGATATTGATGTTGAGGCCATCTTGAAGAAGCTCACCCTGGCCGAGAAGGTCGAT 60
          ||| || |  ||||||||||     | ||||   |  | | || ||  || ||| |

Db    612 ATGTCTAAATTTGATGTTGAACAGTTATTGAGTGAATTGAACCAGGATGAAAAGATTTCC 671

Qy     61 CTGCTGGCTGGTATCGACTTCTGGCACACAAAGGCTCTCCCCAAGCATGGAGTCCCCTCT 120
          | ||  |||   | || |||||||| || |||    |       |   ||| | ||  |

Db    672 TTACTTTCTGCAGTTGATTTCTGGCATACTAAGAAGATTGAACGGTTGGGAATTCCAGCG 731

Qy    121 CTCCGCTTTACAGATGGCCCCAACGGCGTAAGAGGGACCAAGTTCTTCAATGGCGTCCCT 180
          |  |  || | ||||| || || ||  | |||||||| ||||||||  |||| || |||

Db    732 GTGAGGGTTTCTGATGGTCCAAATGGTATTAGAGGGACGAAGTTCTTTGATGGGGTTCCT 791

Qy    181 GCGGCCTGCTTCCCTTGCGGCACGTCGCTCGGTTCCACATTCAACCAAACTCTGCTCGAA 240
          | |  || ||||||   || ||   | | |  || || ||  | |    |||||| ||

Db    792 TCAGGATGTTTCCCTAATGGTACCGGGTTGGCATCTACTTTTGATCGCGATCTGCTTGAG 851

Qy    241 GAGGCAGGTAAGATGATGGGCAAAGAGGCCATCGCTAAGAGTGCGCATGTGATCCTCGGC 300
            |||||||| ||||||  || ||  | || || |||| |||   ||||||  | ||

Db    852 ACAGCAGGTAAGTTGATGGCTAAGGAATCGATTGCGAAGAATGCTGCTGTGATTTTGGGT 911

Qy    301 CCGACTATCAACATGCAACGCTCCCCTCTCGGTGGACGTGGCTTCGAGTCGATTGGTGAG 360
          || || |  ||||||||||||    ||| | ||||| ||||| || || ||  |   |||

Db    912 CCAACCACAAACATGCAACGTGGTCCTTTGGGTGGTCGTGGTTTTGAATCATTCTCTGAA 971

Qy    361 GATCCGTTCCTGGCGGGCTTGGGAGCTGCGGCTCTCATCCGCGGCATTCAGAGCACTGGA 420
          |||||  |  || || ||  |||   || |  || |  |    || || ||  ||   ||

Db    972 GATCCATATCTTGCTGGTATGGCTACTTCTTCTGTTGTTAAAGGTATGCAAGGCGAAGGT 1031

Qy    421 GTGCAGGCTACGATCAAGCACTTTTTGTGCAATGATCAGGAGGACAGGCGCATGATGGTG 480
          |    |||||  | ||||| ||| | || || ||  ||| |||  ||  |      |

Db   1032 ATTGCTGCTACCGTTAAGCATTTTGTTTGTAACGACTTGGAAGACCAACGTTTTTCTTCG 1091

Qy    481 CAGAGCATCGTCACGGAGCGGGCTCTCCGTGAAATCTACGCACTCCCGTTCCAGATTGCT 540
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Db   1092 AACTCAATTGTTTCTGAAAGGGCTCTGAGAGAAATTTACTTGGAGCCCTTCAGATTGGCA 1151

Qy    541 GTGCGAGACTCCCAGCCGGGTGCGTTCATGACGGCGTACAATGGCATCAATGGCGTGTCG 600
          ||   | |  || | || | |    | ||||| || || ||     |||||||||

Db   1152 GTTAAACATGCCAATCCTGTTTGTATAATGACTGCTTATAACAAGGTCAATGGCGATCAT 1211

Qy    601 TGCAGCGAGAACCCTAAATATCTTGATGGGATGCTTCGAAAGGAATGGGGTTGGGATGGC 660
          |||  | |   |   ||      |    |  ||  |  || | || |||   ||||| ||

Db   1212 TGCTCCCAATCCAAGAAGCTATTGATCGACATTTTGAGAGACGAGTGGAAATGGGACGGT 1271

Qy    661 CTAATCATGAGCGACTGGTACGGCACATACAGTACCACAGAAGCCGTTGTGGCAGGCCTC 720
          |  | |||  |||||||| ||| ||||| |  ||  | | |||  |   |   ||  |

Db   1272 ATGTTAATGTCCGACTGGTTCGGTACATATACGACTGCCGCAGCTATCAAGAATGGGTTG 1331

Qy    721 GACCTCGAGATGCCCGGACCTCCACGCTTCCGAGGAGAAACACTCAAGTTCAACGT---- 776
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Db   1332 GATATCGAGTTCCCTGGACCAACAAGATGGAGAACACGTGCTTTAGTGTCTCACTCTCTC 1391

Qy    777 --CTCCAACGGAAAGCCCTTTATCCACGTCATTGACCAGAGGGCTAGGGAAGTTCTTCAG 834
            |||||  | | |   |  ||   | |   ||||  |  | | |||  |||| ||  |

Db   1392 AACTCCAGAGAACAAATCACTACTGAAGATGTTGATGATCGTGTTAGACAAGTGCTAAAA 1451

Qy    835 TTCGTCAAGAAGTGTGCTGCCTCCGGAGTGAC-----------GGAGAACGGCCCCGAG 882
          |  | |||      || || |     || ||             |||||| ||||| ||

Db   1452 ATGATTAAGTTCGTTGTTGACAATTTAGAGAAAACAGGTATTGTGGAGAATGGCCCAGAA 1511

Qy    883 ACGACTGTCAACAACACCCCCGAAACGGCAGCTCTCCTCCGGAAGGTTGGCAACGAGGGC 942
          | |||   |||||||||   |||||  | |  ||  |  |  || |||     ||

Db   1512 TCTACTTCAAACAACACCAAGGAAACCTCGGACCTGTTGAGAGAGATTGCTGCTGACTCT 1571

Qy    943 ATCGTGCTGCTGAAGAACGAGAACAACGTTCTGCCCTTGAGCAAGAAGAAGAAGACGCTG 1002
          || ||  | ||||||| | |||||  |||  |||  |  | |  |   |    |

Db   1572 ATTGTTTTATTGAAGAACAAAAACAATTATCTTACCTCTAAAGAAAGAAGACAATATCAT 1631

Qy   1003 ATTGTCGGCCCCAACGCCAAGCAGGCCACATACCACGGCGGAGGCTCTGCCGCACTCAGG 1062
          |  | |||||  || || ||        ||       |||  || || || || ||  | | |

Db   1632 GTCATTGGCCCAAATGCTAAAGCAAAGACTAGTTCCGGTGGTGGTTCAGCATCTATGAAC 1691

Qy   1063 GCCTACTACGCAGTCACTCCCTTTGACGGCCTCAGCAAGCAGCTCGAGACGCCGCCATCG 1122
          |||||||  |  ||  |||| | ||| ||  ||  |||  ||||  |  |    |

Db   1692 TCCTACTATGTTGTTTCTCCGTATGAAGGTATCGTCAATAAGCTGGGCAAAGAGGTCGAT 1751
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Qy   1123 TACACCGTCGGCGCCTA--CACCACCGTTCCTCCCATTCTAGGCGAGCAGTGCCTCACGC 1180
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Qy   1181 CCGACGGCGCTCCGGGCATGCGCTGGAGGGTCTTCAACGA--GCCCCCTGGTACCCCTAA 1238
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Qy   1239 CCGCCAGCACA----------------------TTGACGAGCTCTTCTTCACCAAGACG 1275
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Qy   1276 GACATGCACCTGGTGGACTACTACCACCCCAAGGCGGCAGACACG---------TGGTAC 1326
Db   1932 AATGTTCACTTATTTGATTTCAAACATGAGAAAGTGGATCCAAAGAACCCTTACTTTTTT 1991

Qy   1327 GCCGACATGGAGGGCACGTACACCGCCGACGAGGACTGCACCTACGAGCTCGGCCTCGTC 1386
Db   1992 GTAACCTTAACCGGACAGTACGTGCCTCAAGAAGATGGTGATTATATCTTCAGTCTTCAA 2051

Qy   1387 GTCTGCGGCACGGCAAAGGCGTACGTAGACGACCAGCTCGTCGTCGACAACGCCACCAAG 1446
Db   2052 GTTTATGGTTCTGGTTTGTTCTACTTAAACGATGAGTTGATTATTGACCAAAAGCACAAC 2111

Qy   1447 CAGGTCCCCGGCGATGCCTTCTTCGGCTCCGCCACCGCGAGGAGACGGGCCGCATCAAT 1506
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Qy   1507 CTCGTCAAGGGCAACACGTACAAGTTCAAGATCGAGTTCGGCTCCGCACCCACCTACACC 1566
Db   2172 TTGAAGAAGGGCCAAGTTTATAATGTAAGAGTTGAGTACGGTTCTGGCCCAACTTCAGGT 2231

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Db   2232 TTGGTTGGGGA---------ATTCGGTGCAGGTGGATTCCAAGCTGGTGTCATTAAGGCG 2282

Qy   1627 ATTGACGACCAGGCCGAAATCGAAAAGTCCGTCGCCCTCGCCAAGGAGCACGACCAGGTC 1686
Db   2283 ATCGATGATGACGAGGAGATTAGAAACGCAGCAGAATTAGCAGCTAAGCATGATAAGGCT 2342

Qy   1687 ATCATCTGCGCGGGCCTTAACGCCGACTGGGAGACCGAGGGCGCCGACCGCGCGAGCATG 1746
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Qy   1747 AAGCTCCCCGGCGTGCTGGACCAGCTCATTGCCGACGTGGCCGCCGCGAACCCAAACACC 1806
Db   2403 GATTTGCCAAAAAGAACAAATGAATTAGTTCGTGCTGTTTTGAAAGCAAATCCAAATACT 2462

Qy   1807 GTCGTCGTCATGCAGACGGGCACCCCCGAGGAGATGCCCTGGCTCGACGCCACGCCCGCC 1866
Db   2463 GTTATCGTTAACCAATCAGGTACCCCAGTTGAGTTCCCTTGGTTAGAAGAGGCAAATGCG 2522

Qy   1867 GTCATCCAGGCCTGGTACGGCGGCAACGAGACGGGCAACTCCATTGCCGACGTCGTCTTT 1926
Db   2523 CTAGTTCAAGCTTGGTACGGTGGTAATGAATTGGGTAATGCTATCGCAGATGTCTTGTAC 2582

Qy   1927 GGCGACTACAACCCCTCGGGCAAGCTGTCCCTCAGCTTCCCCAAGCGCCTGCAGGACAAC 1986
Db   2583 GGTGACGTGGTTCCAAATGGTAAGTTATCGCTCTCTTGGCCATTTAAGTTGCAAGATAAT 2642

Qy   1987 CCCGCGTTTCTCAACTTCCGCACCGAGGCCGGGCGCACGCTGTACGGCGAGGACGTGTAC 2046
Db   2643 CCAGCCTTTTTAAACTTCAAGACCGAGTTCGGAAGAGTTGTTTACGGTGAGGATATCTTT 2702

Qy   2047 GTCGGGTACAGGTACTACGAGTTTGCCGACAAGGACGTCAATTTCCCCTTTGGCCACGGC 2106
Db   2703 GTTGGTTATAGGTACTACGAAAAGCTTCAAAGAAAGGTAGCCTTCCCCTTCGGATATGGT 2762

Qy   2107 CTGTCCTACACCACTTTTGCCTTTTCCAATCTCTCCGTGTCTCACAAGGACGGCAAGCTG 2166
Db   2763 CTATCGTATACAACATTCGAACTAGATATTTCTGACTTCAAGGTAACTGATGATAAGATA 2822

Qy   2167 AGCGTGTCCCTCTCCGTGAAGAACACCGGCTCCGTGCCCGGCGCACAGGTGGCCCAGCTC 2226
Db   2823 GATATTTCAGTTGATGTGAAGAATACTGGTGATAAATTTGCTGGCTCCGAGGTGGTGCAA 2882

Qy   2227 TACGTCAAGCCCCTCCAAGCGGCCAAGATTAACCGCCCCGTCAAGGAGCTCAAGGGCTTC 2286
Db   2883 GTCTACTTCAGCGCTCTAAACTCTAAGGTCTCGAGACCGGTTAAGGAGTTCAAGGGATTC 2942

Qy   2287 GCAAAGGTCGAACTGCAGCCCGGCGAGACGAAGGCGGTGACAATCGAGGAGCAGGAGAAG 2346
Db   2943 GAAAAAGTTCATTTGGAACCAGGTGAGAAGAAGACAGTTAATATTGAACTAGAATTGAAA 3002

Qy   2347 TACGTCGCTGCGTATTTTGATGAGGAGCGGGATCAGTGGTGTGTCGAAAAGGGTGACTAT 2406
Db   3003 GATGCAATTTCCTACTTTAACGAAGAGCTCGGTAAATGGCACGTTGAAGCAGGTGAATAC 3062

Qy   2407 GAGGTTATCGT 2417
Db   3063 TTGGTTTCAGT 3073
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RESULT 2
AF486581

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LOCUS       AF486581                38269 bp    DNA     linear   BCT 21-MAR-2002
DEFINITION  Uncultured bacterium aminoglycoside 3'-N-acetyltransferase gene,
            complete cds.
ACCESSION   AF486581
VERSION     AF486581.1  GI:19569565
KEYWORDS    .
SOURCE      uncultured bacterium.
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 38269)
  AUTHORS   Cappellano,C.M., Courtois,S., Ball,M., Francou,F.-X., Normand,P.,
            Heylinck,G., Guerineau,M., Martinez,A., Hopke,J., Kolvek,S.,
            August,P.R., Osburne,M.S., Jeannin,P., Simonet,P. and
            Pernodet,J.-L.
  TITLE     Recombinant Environmental Libraries Provide Access to Microbial
            Diversity for Natural Products Drug Discovery
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 38269)
  AUTHORS   August,P.R. and Martinez,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-FEB-2002) Molecular Biodiversity, Aventis Cambridge
            Genomics Center, 26 Landsdowne Street, Cambridge, MA 02139, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:77133"
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                     /codon_start=1
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BASE COUNT     6318 a  12117 c  12998 g   6835 t      1 others
ORIGIN

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  Best Local Similarity   50.8%;  Pred. No. 2.7e-40;
  Matches 1213;  Conservative    0;  Mismatches 1098;  Indels   78;  Gaps    7;

Qy        17 TTGAGGCCATCTTGAAGAAGCTCACCCTGGCCGAGAAGGTCGATCTGCTGGCTGGTATCG 76
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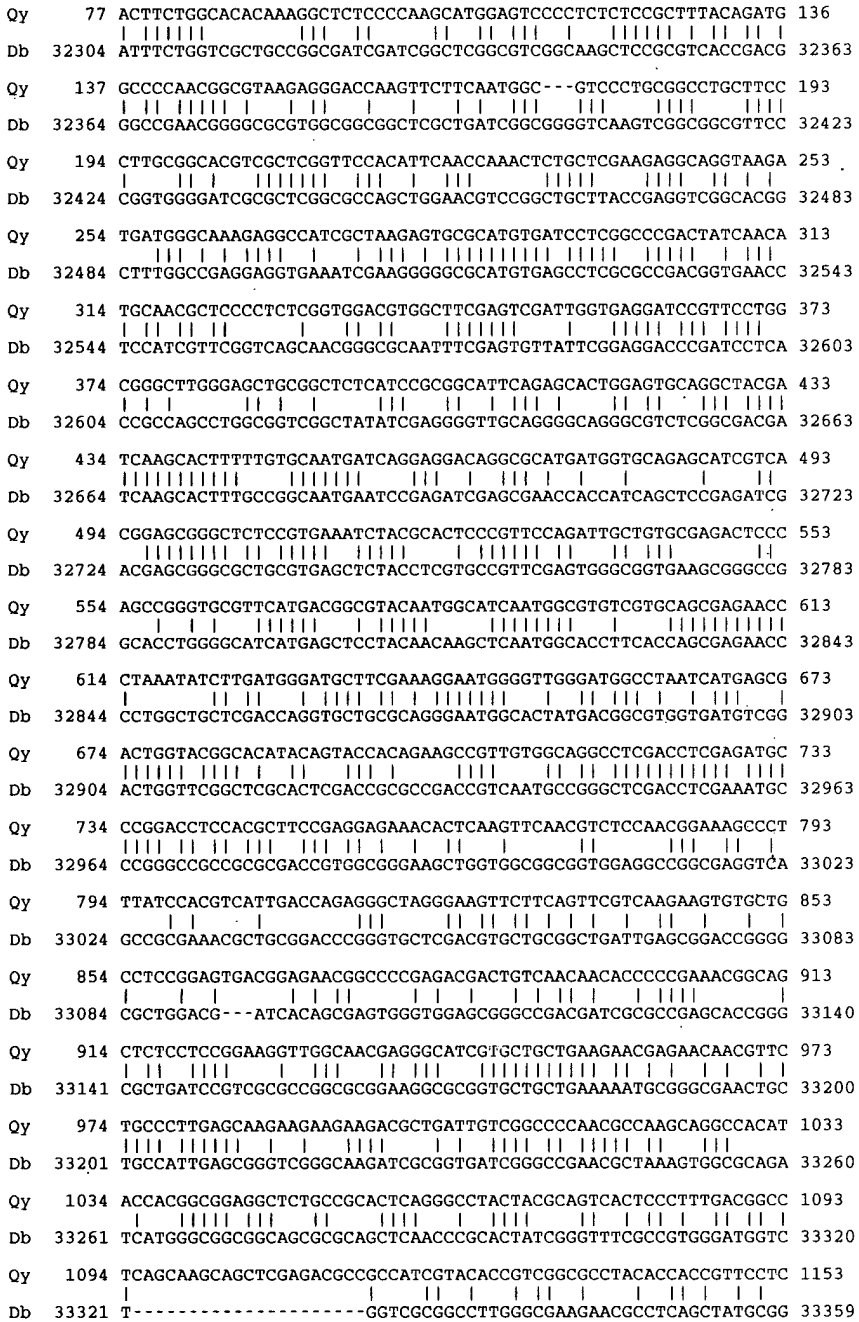
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Db 32304 ATTTCTGGTCGCTGCCGGCGATCGATCGGCTCGGCGTCGGCAAGCTCCGCGTCACCGACG 32363
Qy 137 GCCCCAACGGCGTAAGAGGGACCAAGTTCTTCAATGGC---GTCCCTGCGGCCTGCTTCC 193
Db 32364 GGCCGAACGGGGCGCGTGGCGGCGGCTCGCTGATCGGCGGGGTCAAGTCGGCGGCGTTCC 32423
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Db 32424 CGGTGGGGATCGCGCTCGGCGCCAGCTGGAACGTCCGGCTGCTTACCGAGGTCGGCACGG 32483
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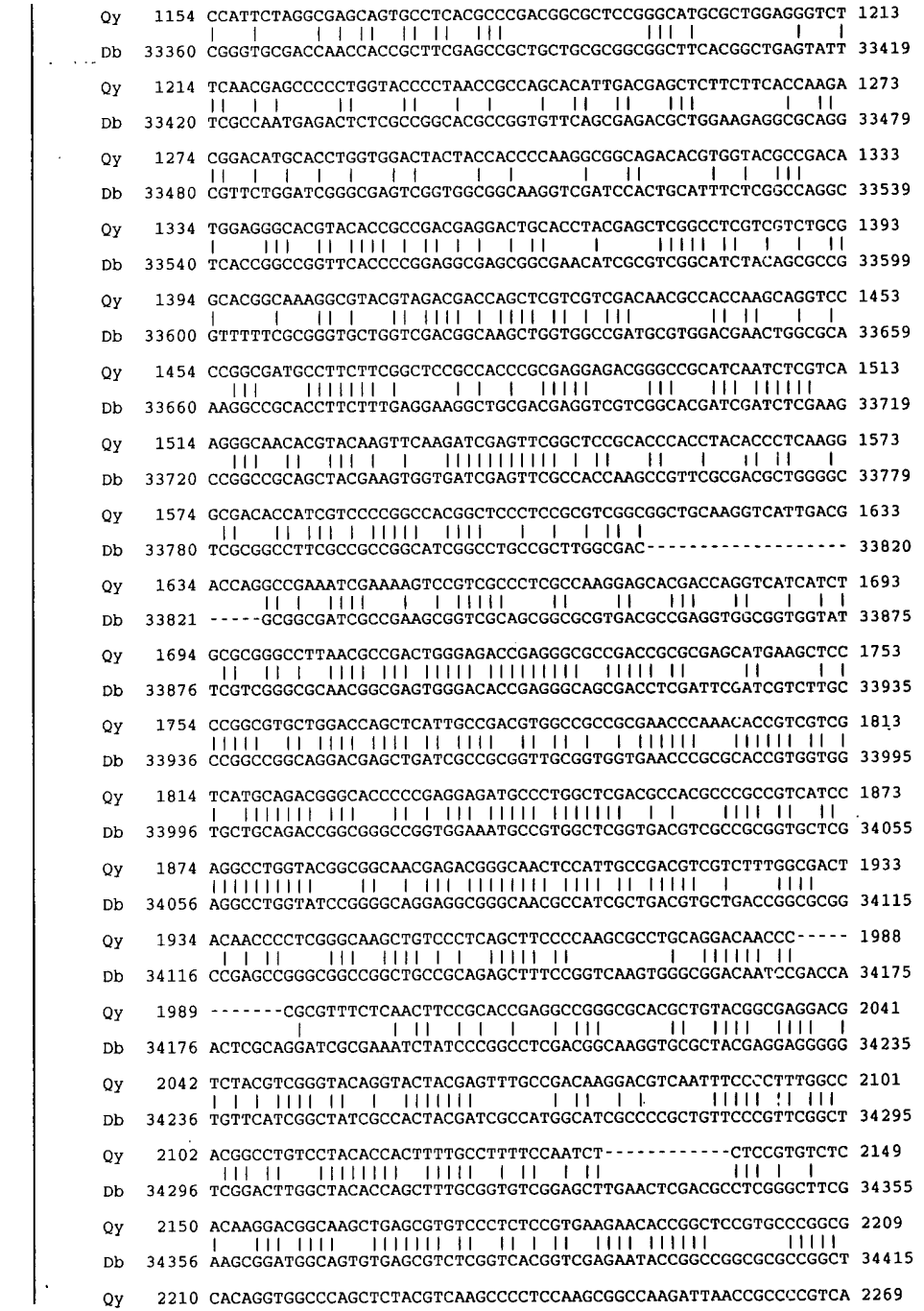
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RESULT 3
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DEFINITION  Schizosaccharomyces pombe cosmid 1683.
ACCESSION   U33009
VERSION     U33009.1  GI:1063616
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe.
  ORGANISM  Schizosaccharomyces pombe
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            Schizosaccharomycetales; Schizosaccharomycetaceae;
            Schizosaccharomyces.
REFERENCE   1  (bases 1 to 39305)
  AUTHORS   McCombie,W.R.
  TITLE     Sequence analysis of a region of the fission yeast genome
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 39305)
  AUTHORS   McCombie,W.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-1995) W. Richard McCombie, Cold Spring Harbor
            Lab, 1 Bungtown Rd, P.O. Box 100, Cold Spring Harbor, NY 11754, USA
FEATURES             Location/Qualifiers
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ORIGIN

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Qy      61 CTGCTGGCTGGTATCGACTTCTGGCACACAAAGGCTCTCCCCAAGCATGGAGTCCCCTCT 120
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Qy     121 CTCCGCTTTACAGATGGCCCCAACGGCGTAAGAGGGACCAAGTTCTTCAATGGCGTCCCT 180
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Qy     241 GAGGCAGGTAAGATGATGGGCAAAGAGGCCATCGCTAAGAGTGCGCATGTGATCCTCGGC 300
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Qy     361 GATCCGTTCCTGGCGGGCTTGGGAGCTGCGGCTCTCATCCGCGGCATTCAGAGCACTGGA 420
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Qy     421 GTGCAGGCTACGATCAAGCACTTTTTGTGCAATGATCAGGAGGACAGGCGCATGATGGTG 480
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Qy     481 CAGAGCATCGTCACGGAGCGGGCTCTCCGTGAAATCTACGCACTCCCGTTCCAGATTGCT 540
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Db    9277 GGATCCAAAGAGCTTTCGGAGTCAATTTTAGATGAAAGAGCAAAGAATGTCCTGAAGCTT 9336

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Qy    1252 GACGAGCTCTTCTTCACCAAGACGGACATGCACCTGGTGGACTACTACCACCCCAA---G 1308
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Db    9874 TATGAATTTGGGATATCTGTGTTTGGAACGGCTCTGCTGTTTATTGATGATGTCTTATTA 9933

Qy    1429 GTCGACAACGCCACCAAGCAGGTCCCCGGCGATGCCTTCTTCGGCTCCGCCACCCGCGAG 1488
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Qy   1669 AAGGAGCACGACCAGGTCATCATCTGCGCGGGCCTTAACGCCGACTGGGAGACCGAGGGC 1728
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Qy   1849 CTCGACGCCACGCCCGCCGTCATCCAGGCCTGGTACGGCGGCAACGAGACGGGCAACTCC 1908
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Qy   2029 TACGGCGAGGACGTCTACGTCGGGTACAGGTACTACGAGTTTGCCGACAAGGACGTCAAT 2088
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Qy   2089 TTCCCCTTTGGCCACGGCCTGTCCTACACCACTTTTGCCTTTTCCAATCTCTCCGTGTCT 2148
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Qy   2329 ATCGAGGAGCAGGAGAAGTACGTCGCTGCGTATTTTGATGAGGAGCGGGATCAGTGGTGT 2388
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RESULT 4
SPBC1683
LOCUS SPBC1683 41799 bp DNA linear PLN 23-AUG-2000
DEFINITION Schizosaccharomyces pombe cosmids c1683.
ACCESSION AL355920
VERSION AL355920.1 GI:7801293
KEYWORDS adenosine deaminase; alpha-glucosidase; beta-glucosidase precursor (EC 3.2.1.21); ferric reductase transmembrane component; frp1; ght4; glucose transporter protein; glycosyl hydrolase family 3; inosine-uridine preferring nucleoside hydrolase; isocitrate lyase (EC 4.1.3.1); MFS allantoate permease; MFS inorganic phosphate transporter; MFS transporter of unkown specificity; NCS1 allantoate transporter; TF1-type LTR; transcriptional activator; zinc finger.
SOURCE fission yeast.
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE 1 (bases 1 to 41799)
AUTHORS McCombie,W.R.
TITLE Sequence analysis of a region of the fission yeast genome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 41799)
AUTHORS McCombie,W.R. and Lyne,M.H.
TITLE Direct Submission
JOURNAL Submitted (11-APR-2000) W. Richard McCombie, Cold Spring Harbor Lab, 1 Bungtown Rd, P.O. Box 100, Cold Spring Harbor, NY 11754, USA and Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA
COMMENT Notes:
Details of yeast sequencing at the Sanger Centre are available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand).
The length in codons is given for each CDS.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
Cosmid SPBC1683 is overlapped at its 5' end by cosmid SPBC359 and at its 3' end by cosmid SPBC1198.

FEATURES Location/Qualifiers

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Qy     61 CTGCTGGCTGGTATCGACTTCTGGCACACAAAGGCTCTCCCCAAGCATGGAGTCCCCTCT 120
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Qy    181 GCGGCCTGCTTCCCTTGCGGCACGTCGCTCGGTTCCACATTCAACCAAACTCTGCTCGAA 240
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Qy    241 GAGGCAGGTAAGATGATGGGCAAAGAGGCCATCGCTAAGAGTGCGCATGTGATCCTCGGC 300
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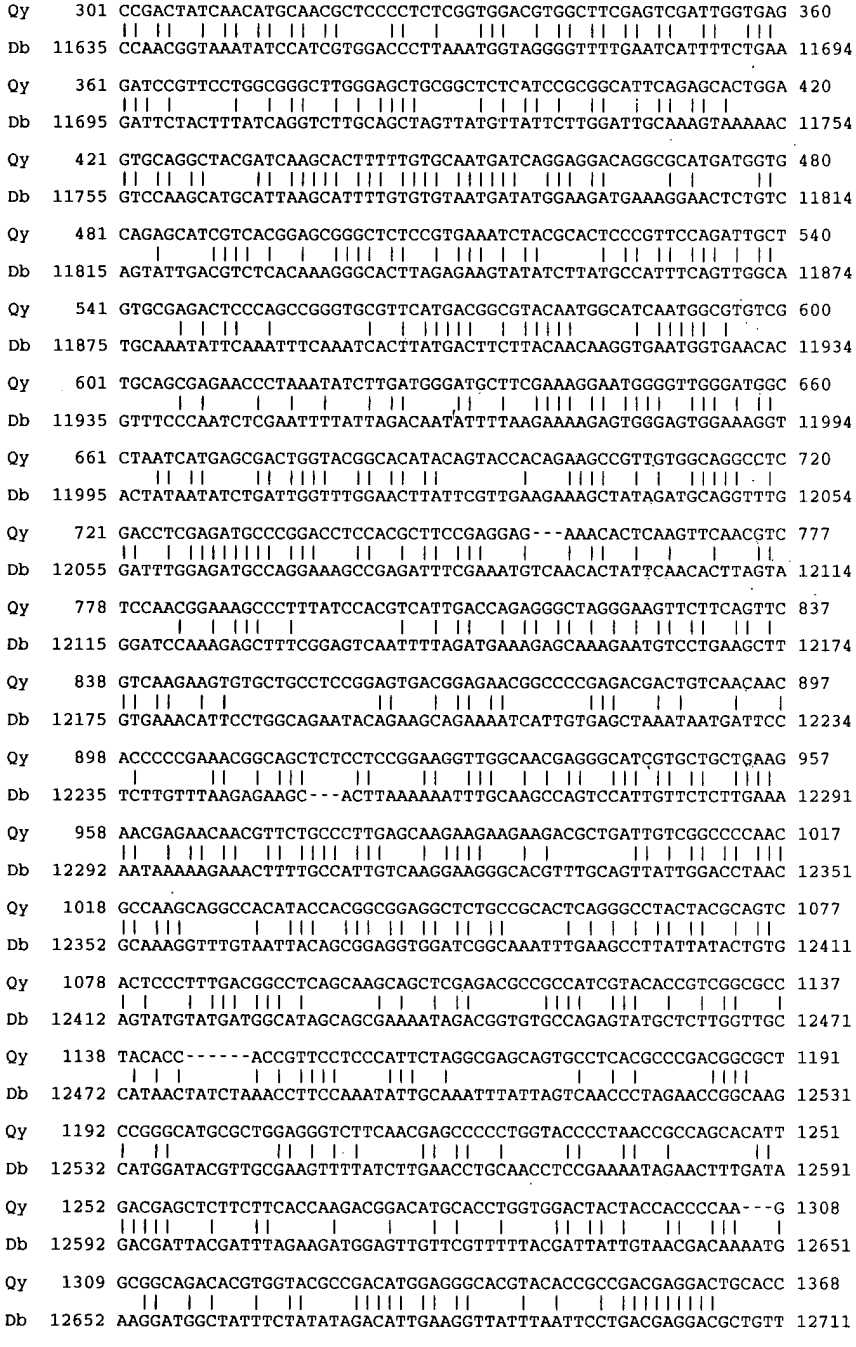
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DEFINITION  Schizosaccharomyces pombe cosmids 359, 1198 and 1683.
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VERSION     U33010.1  GI:1063617
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SOURCE      Schizosaccharomyces pombe.
  ORGANISM  Schizosaccharomyces pombe
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            Schizosaccharomycetales; Schizosaccharomycetaceae;
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REFERENCE   1  (bases 1 to 85837)
  AUTHORS   McCombie,W.R.
  TITLE     Sequence analysis of a region of the fission yeast genome
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 85837)
  AUTHORS   McCombie,W.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-1995) W. Richard McCombie, Cold Spring Harbor
            Lab, 1 Bungtown Rd, P.O. Box 100, Cold Spring Harbor, NY 11754, USA
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Qy        481 CAGAGCATCGTCACGGAGCGGGCTCTCCGTGAAATCTACGCACTCCCGTTCCAGATTGCT 540
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Qy   1789 GCCGCGAACCCAAACACCGTCGTCGTCATGCAGACGGGCACCCCCGAGGAGATGCCCTGG 1848
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Db  30913 CAATCCAATCCCAATACAGTAGTTGTGACTCAATCAGGCACTCCAATTGAGATGCCATGG 30972

Qy   1849 CTCGACGCCACGCCCGCCGTCATCCAGGCCTGGTACGGCGGCAACGAGACGGGCAACTCC 1908
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Db  30973 ATCTCTGAAGCCCACACCTTATTGCACATTTGGTACAACGGTAACGAATTAGGAAATGCT 31032

Qy   1909 ATTGCCGACGTCGTCTTTGGCGACTACAACCCCTCGGGCAAGCTGTCCCTCAGCTTCCCC 1968
          | ||  || |  | ||||| ||  | ||||| |  || ||  || |  | |  |||||
Db  31033 TTAGCAAACATTATTTTTGGAGAGCAAAACCCTTGTGGAAAATTGCCAATAACATTCCCT 31092

Qy   1969 AAGCGCCTGCAGGACAACCCCGCGTTTCTCAACTTCCGCACCGAGGCCGGGCGCACGCTG 2028
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Db  31093 AAAAAACTGAAGGATAATCCTGCCTATCTTTCATTTCGTTCAAGCCGTGGCCATTGTGTT 31152

Qy   2029 TACGGCGAGGACGTCTACGTCGGGTACAGGTACTACGAGTTTGCCGACAAGGACGTCAAT 2088
          || || || |||||||  || ||||| | ||| || ||    |  || | ||| |||
Db  31153 TATGGAGAAGACGTCTTTGTTGGGTATAAGTATTATGAAGCCGTAGAAAGGGAGGTCTTG 31212

Qy   2089 TTCCCCTTTGGCCACGGCCTGTCCTACACCACTTTTGCCTTTTCCAATCTCTCCGTGTCT 2148
          || || |||||  | || || || || || |||||||  || ||||||| |   ||
Db  31213 TTTCCATTTGGATATGGGCTTTCATATACTACTTTTGAATTATCCAATCTTTATTTGAAG 31272

Qy   2149 CACAAGGACGGCAAGCTGAGCGTGTCCCTCTCCGTGAAGAACACCGGCTCCGTGCCCGGC 2208
           |    |  |  | | | ||  |      |      |   ||| || ||| || || | ||
Db  31273 AATTGTGGTGAAAGGTTAAGGATCGATTTGGAGATTTCGAATACTGGCCCCATGTCTGGT 31332

Qy   2209 GCACAGGTGGCCCAGCTCTACGTCAAGCCCCTCCAAGCGGCCAAGATTAACCGCCCCGTC 2268
          ||| |  |    ||  | ||  |    |   ||   |          |||| || || ||
Db  31333 GCAGAAATTATACAAGTATATATTTCTCAAATC---GTTCGTTCAGTTAATCGACCTGTT 31389

Qy   2269 AAGGAGCTCAAGGGCTTCGCAAAGGTCGAACTGCAGCCCGGCGAGACGAAGGCGGTGACA 2328
          || || || || |  ||  | || || |    |    ||    ||||| ||      | | |
Db  31390 AAAGAACTAAAAGAGTTTTCTAAAGTGGTTTTATGTCCTAAAGAGACCAAATTAATTAGA 31449

Qy   2329 ATCGAGGAGCAGGAGAAGTACGTCGCTGCGTATTTTGATGAGGAGCGGGATCAGTGGTGT 2388
          || |||  | |    |||||  |   || | | || ||||||        ||  | ||||||
Db  31450 ATTGAGTTGGATATAAAGTATGCTACTTCTTTTTATGATGAACTTAATGAAAAATGGTGT 31509

Qy   2389 GTCGAAAAGGGTGACTATGAGGTTATCGTGAGCGACAGCAGCGCAG 2434
            ||| |||| || ||  | ||| | ||  |   ||||||   ||
Db  31510 TCTGAAGAGGGCGAGTACAACGTTCTTGTCGGAACCAGCAGTAAAG 31555
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RESULT 6
AF329731

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LOCUS       AF329731               2793 bp    mRNA    linear   PLN 28-JAN-2001
DEFINITION  Volvariella volvacea beta-glucosidase mRNA, complete cds.
ACCESSION   AF329731
VERSION     AF329731.1  GI:12584216
KEYWORDS    .
SOURCE      Volvariella volvacea.
  ORGANISM  Volvariella volvacea
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
            Agaricales; Pluteaceae; Volvariella.
REFERENCE   1  (bases 1 to 2793)
  AUTHORS   Ding,S., Ge,W. and Buswell,J.A.
  TITLE     Molecular cloning, characterization and expression of a
            beta-glucosidase gene from the edible straw mushroom, Volvariella
            volvacea
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2793)
  AUTHORS   Ding,S., Ge,W. and Buswell,J.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-DEC-2000) Biology, The Chinese University of Hong
            Kong, Shatin, N.T., Hong Kong, China
FEATURES             Location/Qualifiers
     source          1. .2793
                     /organism="Volvariella volvacea"
                     /strain="V14"
                     /db_xref="taxon:36659"
     CDS             41. .2629
                     /EC_number="3.2.1.21"
                     /codon_start=1
                     /product="beta-glucosidase"
                     /protein_id="AAG59831.1"
                     /db_xref="GI:12584217"
                     /translation="MPPSDFAKANIDEIVEQLTLDEAISLTAGVGFWHTHAIERLGVP
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                     LVLAPTSNIQRNPLGGRSFESFSEDPYLSGIISASYVNGVQKGGIGATIKHFVGNDKE
                     DDRQGYDSIISERALREIYLLPFMLTQKYAAPWAIMTAYNRVNGVHVAEDPFLLKQVL
                     RNEWKYKGLIMSDWFGMYSVDHGIKAGLDLEMPGINKWRTLDLVNRTIQARKLTPRDI
                     KDRARVVLELVKKCAQGAPEILDGDGEERTVELESDKLLMRRIASESIVLLKNDNVLP
                     LKPEGGAIKKIAVVGGNAKAQVLSGGGSAALKASYFISPYDGIKAALEPHGVEVTFSE
                     GARAYKTLPTLEWDLETETGERGWIGTWHTHESDDSMTALDQPFIAPRLVDETRIFIS
                     TSYPKGITKRWTMRLKGYLKPREKDTNFEFGLIAAGRAKLWVDGQLVIDNWTRQRRGE
                     AFFGSGSQEETGVYLLKAGKKHEIYVEYCNVRAPADGDEDEAIMDSNPGVRLGGAEVA
                     NADDLLSEAVKLASEADAVIAVVGLNADWETEGNDRRTLALPGRTDELVEKVAKVNSK
                     TVVVTQAGSAITLPWLDSVAAVVHAWYLGNATGDAIADVLFGKQNPSGKLSLTFPKRL
                     EDVPSHGHFGSENGKVRYAEDLFVGYKHYHHRNIEPLFPFGFGLSYTTFSLSNLQLSA
                     PVIDHATSSFSLTATLSITNTGPVTGSEVAQLYVSYPETSELTHAPLQLRAFKKVKDL
                     QPGETREVKLELDKYAVSYWNDRYQTWAVENGEYEIKVGNSSVSKDLTLVQRFVVKDG
                     FEWRGI"
BASE COUNT      697 a    696 c    737 g    663 t
ORIGIN
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Query Match 15.7%; Score 392.2; DB 8; Length 2793;
Best Local Similarity 50.3%; Pred. No. 2.6e-38;
Matches 1258; Conservative 0; Mismatches 1168; Indels 75; Gaps 9;

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Qy     17 TTGAGGCCATCTTGAAGAAGCTCACCCTGGCCGAGAAGGTCGATCTGCTGGCTGGTATCG 76
          |||| |  ||| |  || |  | || || |  |||    ||  ||||   |||||| |||
Db     72 TTGATGAAATCGTCGAGCAATTGACGCTCGATGAGGCCATCAGTCTGACCGCTGGTGTCG 131

Qy     77 ACTTCTGGCACACAAAGGCTCTCCCCAAGCATGGAGTCCCCTCTCTCCGCTTTACAGATG 136
          ||||||||  ||  | ||  |        |  || || ||  || |    | |  ||||
Db    132 GTTTCTGGCATACGCATGCGATTGAGCGTCTCGGTGTGCCAGCTGTAAAGGTCAGCGATG 191

Qy    137 GCCCCAACGGCGTAAGAGGGACCAAGTTCTTCAATGGCGTCCCTGCGGCCTGCTTCCCTT 196
          | || |||||| |  |||| | | | |||||||  ||   ||||||    ||  | ||||
Db    192 GACCAAACGGCATTCGAGGCAACCACTTCTTCATGGGGACCCCTGCAAAATGTCTACCTT 251

Qy    197 GCGGCACGTCGCTCGGTTCCACATTCAACCAAACTCTGCTCGAAGAGGCAGG---TAAGA 253
          |   ||  | || ||  | || |   |||      |  |||| |||| ||    |||
Db    252 CCTCAACCGCTCTTGGCGCAACTTGGGACCCTGAAGTCGTCGAGGAGGTCAGGTTGAAGC 311

Qy    254 TGATGGGCAAAGAGGCCATCGCTAAGAGTGCGCATGTGATCCTCGGCCCGACTATCAACA 313
          |  | | |   || || |           ||   | |  | || |  || ||| |||||
Db    312 TCCTAGCCCCTGAAGCTAAGCTGCGAGCGGCTTCTCTAGTTCTTGCTCCTACTTCCAACA 371

Qy    314 TGCAACGCTCCCCTCTCGGTGGACGTGGCTTCGAGTCGATTGGTGAGGATCCGTTCCTGG 373
          | ||| |   ||| || || || ||| | ||||||     |   |||||||| | |||
Db    372 TCCAAAGAAACCCCCTGGGAGGCCGTAGTTTCGAGAGTTTCTCTGAGGATCCCTACCTTT 431

Qy    374 CGGGCTTGGGAGCTGCGGCTCTCATCCGCGGCATTCAGAGCACTGGAGTGCAGGCTACGA 433
          ||||  |     | ||| |   | ||   ||  | ||||    |||| |    ||||| |
Db    432 CGGGTATCATTTCGGCGTCCTACGTCAATGGTGTGCAGAAGGGTGGAATTGGTGCTACTA 491

Qy    434 TCAAGCACTTTTTGTGCAATGATCAGGAGGACAGGCGCATGATGGTGCAGAGCATCGTCA 493
          |||| || ||| |  | || ||  ||||||||  ||           | || ||  |||
Db    492 TCAAACATTTTGTCGGAAACGACAAGGAGGACGATCGTCAAGGATACGATAGTATTATCA 551

Qy    494 CGGAGCGGGCTCTCCGTGAAATCTACGCACTCCCGTTCCAGATTGCTGTGCGAGACTCCC 553
            || || |||||||| ||||||||   |||||| ||   | |  ||        | |
Db    552 GCGAACGTGCTCTCCGCGAAATCTATCTACTCCCTTTTATGTTAACTCAAAAGTATGCTG 611
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Qy    554 AGCCGGGTGCGTTCATGACGGCGTACAATGGCATCAATGGCGTGTCGTGCAGCGAGAACC 613
Db    612 CCCCATGGGCAATCATGACCGCCTACAACCGAGTGAACGGCGTTCATGTAGCGGAAGACC 671

Qy    614 CTAAATATCTTGATGGGATGCTTCGAAAGGAATGGGGTTGGGATGGCCTAATCATGAGCG 673
Db    672 CCTTCCTGCTCAAGCAGGTCCTACGTAATGAGTGGAAATACAAGGGATTGATCATGAGTG 731

Qy    674 ACTGGTACGGCACATACAGTACCACAGAAGCCGTTGTGGCAGGCCTCGACCTCGAGATGC 733
Db    732 ACTGGTTCGGCATGTACAGCGTTGATCATGGTATCAAGGCCGGTCTAGACCTCGAAATGC 791

Qy    734 CCGGACCTCCACGCTTCCGAGGA---GAAACACTCAAGTTCAACGTCTCCAACGGAAAGC 790
Db    792 CTGGCATCAATAAATGGCGTACACTTGATCTAGTCAACCGTACTATTCAAGCTCGCAAAC 851

Qy    791 CCTTTATCCACGTCATTGACCAGAGGGCTAGGGAAGTTCTTCAGTTCGTCAAGAAGTGTG 850
Db    852 TCACCCCACGAGACATCAAGGACCGAGCACGAGTTGTATTAGAGTTAGTCAAGAAGTGTG 911

Qy    851 CT------GCCTCCGGAGTGACGGAGAACGGCCCCGAGACGACTGTCAACAACACCCCCG 904
Db    912 CTCAAGGAGCCCCAGAGATTCTCGATGGCGATGGCGAGGAGCGTACAGTCGAGCTTGAAT 971

Qy    905 AAACGGCAGCTCTCCTCCGGAAGGTTGGCAACGAGGGCATCGTGCTGCTGAAGAACGAGA 964
Db    972 CCGACAAGCTGCTCATGCGGCGCATCGCATCTGAGTCCATCGTCCTACTCAAAAATGATA 1031

Qy    965 ACAACGTTCTGCCCT---------TGAGCAAGAAGAAGAAGACGCTGATTGTCGGCCCCA 1015
Db   1032 ACGTTCTCCCTCTTAAACCTGAAGGAGGCGCGATCAAGAAGATCGCCGTCGTTGGTGGCA 1091

Qy   1016 ACGCCAAGCAGGCCACATACCACGGCGGAGGCTCTGCCGCACTCAGGGCCTACTACGCAG 1075
Db   1092 ATGCAAAGGCGCAAGTCCTGTCCGGCGGAGGGTCTGCGGCGCTGAAGGCGTCATACTTCA 1151

Qy   1076 TCACTCCCTTTGACGGCCTCAGCAAGCAGCTCGAGACGCCGCCATCGTACACC------- 1128
Db   1152 TCTCACCCTACGACGGTATTAAGGCCGCCCTCGAACCTCATGGCGTAGAGGTCACATTCA 1211

Qy   1129 --------GTCGGCGCCTACACCACCGTTCCTCCCATTCTAGGCGAGCAGTGCCTCACGC 1180
Db   1212 GTGAGGGTGCTCGAGCCTATAAAACACTACCCACCCTCGAATGGGATCTGGAAACCGAGA 1271

Qy   1181 CCGACGGCGCTCCGGGCATGCGCTGGAGGGTCTTCAACGAGCCCCCTGGTA--------- 1231
Db   1272 CCGGCGAACGTGGATGGATTGGAACGTGGCACACCCACGAGTCCGACGACAGCATGACGG 1331

Qy   1232 CCCCTAACCGCCAGCACATTGACGAGCTCTTCTTCACCAAGACGGACATGCACCTGGTGG 1291
Db   1332 CTCTTGACCAGCCATTCATCGCTCCCCGATTGGTTGACGAAACCAGAATCTTCATCAGCA 1391

Qy   1292 ACTACTACCACCCCAAGGCGGCAGACACGTGGTACGCCGACATGGAGGG---CACGTACA 1348
Db   1392 CGTCGTATCCCAAGGGAATTACAAAGAGGTGGACGATGAGACTGAAGGGCTACCTGAAGC 1451

Qy   1349 CCGCCGACGAGGACTGCACCTACGAGCTCGGCCTCGTCGTCTGCGGCACGGCAAAGGCGT 1408
Db   1452 CAAGAGAGAAGGACACCAACTTCGAATTTGGTCTTATTGCTGCTGGTCGGGCTAAGCTCT 1511

Qy   1409 ACGTAGACGACCAGCTCGTCGTCGACAACGCCACCAAGCAGGTCCCCGGCGATGCCTTCT 1468
Db   1512 GGGTTGACGGACAACTGGTAATCGACAACTGGACCCGTCAACGTCGTGGTGAAGCATTCT 1571

Qy   1469 TCGGCTCCGCCACCCGCGAGGAGACGGGCCGCATCAATCTCGTCAAGGGCAACACGTACA 1528
Db   1572 TTGGCAGTGGTAGTCAGGAGGAAACTGGGGTCTATCTCCTCAAGGCTGGCAAGAAGCATG 1631

Qy   1529 AGTTCAAGATCGAGTTCGGCTC------CGCACCCACCTACACCCTCAAGGGCGACACCA 1582
Db   1632 AAATCTATGTCGAGTACTGTAATGTGCGCGCTCCGGCTGATGGTGATGAAGATGAGGCCA 1691

Qy   1583 TCGTCCCCGGCCACGGCTCCCTCCGCGTCGGCGGCTGCAAGGTCATTGACGACCAGGCCG 1642

Db   1692 TTATGGATAGTAACCCTGGTGTTCGCCTTGGTGGTGCAGAGGTTGCCAACGCAGATGATC 1751

Qy   1643 AAATCGAAAAGTCCGTCGCCCTCGCCAAGGAGCACGACCAGGTCATCATCTGCGCGGGCC 1702
Db   1752 TCCTATCTGAGGCTGTCAAACTTGCTTCAGAGGCTGATGCCGTCATTGCGGTCGTTGGCC 1811

Qy   1703 TTAACGCCGACTGGGAGACCGAGGGCGCCGACCGCGCGAGCATGAAGCTCCCCGGCGTGC 1762
Db   1812 TCAACGCAGATTGGGAGACTGAGGGTAATGACAGAAGGACATTGGCTCTTCCTGGGCGAA 1871

Qy   1763 TGGACCAGCTCATTGCCGACGTGGCCGCCGCGAACCCAAACACCGTCGTCCTCATGCAGA 1822
Db   1872 CGGATGAATTAGTTGAGAAGGTCGCCAAGGTCAACTCGAAGACTGTTGTAGTTACCCAAG 1931

Qy   1823 CGGGCACCCCCGAGGAGATGCCCTGGCTCGACGCCACGCCCGCCGTCATCCAGGCCTGGT 1882
Db   1932 CTGGTTCAGCTATAACTTTGCCATGGCTCGACTCTGTCGCTGCAGTCGTTCACGCATGGT 1991

Qy   1883 ACGGCGGCAACGAGACGGGCAACTCCATTGCCGACGTCGTCTTTGGCGACTACAACCCCT 1942
Db   1992 ATCTTGGTAATGCTACTGGAGATGCTATTGCGGACGTGCTGTTCGGCAAGCAGAATCCAT 2051

Qy   1943 CGGGCAAGCTGTCCCTCAGCTTCCCCAAGCGCCTGCAGGACAACCCCGCGTTTCTCAACT 2002
Db   2052 CTGGTAAATTGTCGTTGACATTCCCTAAGAGGTTGGAGGACGTGCCTTCGCATGGACACT 2111

Qy   2003 TCCGCACCGAGGCCGGGCGCACGCTGTACGGCGAGGACGTCTACGTCGGGTACAGGTACT 2062
Db   2112 TCGGTTCCGAGAACGGCAAGGTACGATATGCCGAAGACTTGTTCGTTGGTTACAAGCACT 2171

Qy   2063 ACGAGTTTGCCGACAAGGACGTCAATTTCCCCTTTGGCCACGGCCTGTCCTACACCACTT 2122
Db   2172 ACCACCACCGCAACATCGAGCCTCTTTTCCCCTTCGGCTTTGGTCTCTCCTACACCACAT 2231

Qy   2123 TTGCCTTTTCCAATCTCTCCGTGT----------CTCACAAGGACGGCA 2161
Db   2232 TCTCCCTCTCCAATCTTCAACTCTCGGCACCAGTCATTGATCATGCAACCTCATCCTTCT 2291

Qy   2162 AGCTGAGCGTGTCCCTCTCCGTGAAGAACACCGGCTCCGTGCCCGGCGCACAGGTGGCCC 2221
Db   2292 CTCTCACCGCAACCCTTTCCATCACCAACACCGGTCCCGTTACCGGCTCCGAAGTCGCCC 2351

Qy   2222 AGCTCTACGTCAAGCCCCTCCAAGCGGCCAAGATTAACCGCCCCGTCAAGGAGCTCAAGG 2281
Db   2352 AACTCTACGTCAGCTATCCCGAAACCTCGGAACTGACACACGCACCACTACAGCTGAGGG 2411

Qy   2282 GCTTCGCAAAGGTCGAACTGCAGCCCGGCGAGACGAAGGCGGTGACAATCGAGGAGCAGG 2341
Db   2412 CGTTCAAGAAGGTGAAGGACTTGCAGCCTGGCGAGACTCGCGAGGTGAAGCTGGAGCTGG 2471

Qy   2342 AGAAGTACGTCGCTGCGTATTTTGATGAGGAGCGGGATCAGTGGTGTGTCGAAAAGGGTG 2401
Db   2472 ACAAATATGCTGTGTCGTATTGGAATGACAGGTATCAGACCTGGGCTGTGGAGAACGGGG 2531

Qy   2402 ACTATGAGGTTATCGTGAGCGACAGCAGCGCAGCGAAGGAT 2442
Db   2532 AGTATGAGATCAAGGTTGGAAATAGCAGCGTGTCAAAGGAT 2572
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RESULT 7
AF005277

LOCUS	AF005277	3578 bp DNA linear BCT 02-MAR-1998
DEFINITION	Cellulomonas biazotea cellobiase (cba) gene, complete cds.	
ACCESSION	AF005277	
VERSION	AF005277.1 GI:2921739	
KEYWORDS	.	
SOURCE	Cellulomonas biazotea.	
ORGANISM	Cellulomonas biazotea Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Cellulomonadaceae; Cellulomonas.	
REFERENCE	1 (bases 1 to 3578)	
AUTHORS	Wong,W.K., Ali,A., Chan,W.K., Ho,V. and Lee,N.T.	

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  TITLE     The cloning, expression and characterization of a cellobiase gene
            encoding a secretory enzyme from Cellulomonas biazotea
  JOURNAL   Gene 207 (1), 79-86 (1998)
  MEDLINE   98172737
   PUBMED   9511746
REFERENCE   2  (bases 1 to 3578)
  AUTHORS   Wong,W.-K.R., Ali,A., Chan,R.W.K., Ho,V. and Lee,N.T.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAY-1997) Biochemistry, The Hong Kong University of
            Science and Technology, Clear Water Bay Road, Kowloon, Hong Kong
FEATURES             Location/Qualifiers
     source          1. .3578
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                     /strain="ATCC 486"
                     /db_xref="ATCC:486"
                     /db_xref="taxon:1709"
     gene            327. .2813
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                     /gene="cba"
                     /function="hydrolyzing beta-D-glucoside and cellobiose"
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                     /codon_start=1
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                     /product="cellobiase"
                     /protein_id="AAC38196.1"
                     /db_xref="GI:2921740"
                     /translation="MTSQTALDPAALVASLPLETKVRLLTGATAFTLAPEESIGLGEV
                     RLSDGPTGVRGLKFSGGRTVALFPNATLLASAWSEESTTEVGRLLAEEALAQQIHVVL
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                     AGEGALEVGAIGVGRWQVTAGGTELAWTLATSGTGFAEEMLAPPTRTDQVHVGSDAVV
                     DATVVLRSSTRSVTVGDADPGTDAGAAAEPLAGVGLFGLVARPAPEAEDDVITRAAAA
                     AAQADVAVVVVGLTEEEETESVDKSTIALPGAQDALVRAVAAAARRTVVVVNAATPVL
                     MPWLDDVDAVLWAGLPGQEGGHAVAAALLGDQEPTGRLVTTFPAADGAAPAWSVTPVD
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                     NTGARTSREVVQVYLEPASSDEPVRLVGWADATVDAGASARVTVTADARMWRRWDEAA
                     GGWSRLADGGRLLVARGLGDVRATLALPTA"
BASE COUNT      426 a   1421 c   1306 g    425 t
ORIGIN

  Query Match             14.0%;  Score 350.4;  DB 1;  Length 3578;
  Best Local Similarity   48.7%;  Pred. No. 2.5e-33;
  Matches 1087;  Conservative    0;  Mismatches 1121;  Indels   24;  Gaps    4;

Qy    109 GGAGTCCCCTCTCTCCGCTTTACAGATGGCCCCAACGGCGTAAGAGGGACCAAGTTCTTC 168
Db    444 GGCCTCGGCGAGGTCCGCCTGTCCGACGGCCCGACCGGCGTGCGCGGCCTCAAGTTCTCC 503

Qy    169 AATGGCGTCCCTGCGGCCTGCTTCCCTTGCGGCACGTCGCTCGGTTCCACATTCAACCAA 228
Db    504 GGCGGGCGCACCGTCGCGCTGTTCCCCAACGCGACCCTGCTCGCGTCCGCGTGGAGCGAG 563

Qy    229 ACTCTGCTCGAAGAGGCAGGTAAGATGATGGGCAAAGAGGCCATCGCTAAGAGTGCGCAT 288
Db    564 GAGTCGACGACCGAGGTCGGCCGGCTGCTCGCCGAGGAGGCCCTCGCGCAGCAGATCCAC 623

Qy    289 GTGATCCTCGGCCCGACTATCAACATGCAACGCTCCCCTCTCGGTGGACGTGGCTTCGAG 348
Db    624 GTCGTGCTCGGCCCCACGATCAACCTGCACCGCTCCGTGCTCGGCGGACGCCTGTTCGAG 683

Qy    349 TCGATTGGTGAGGATCCGTTCCTGGCGGGCTTGGGAGCTGCGGCTCTCATCCGCGGCATT 408
Db    684 GCCTACTCCGAGGACCCGCTGCTCACCGGCCGGCTCGCCGCCGCCTACGTGCGCGGCCTG 743

Qy    409 CAGAGCACTGGAGTGCAGGCTACGATCAAGCACTTTTTGTGCAATGATCAGGAGGACAGG 468
Db    744 CAGGACCTCGGCGTCGGCGCCTGCCTCAAGCACCTCGTCGCCAACGAGTCGGAGACCGAG 803

Qy    469 CGCATGATGGTGCAGAGCATCGTCACGGAGCGGGCTCTCCGTGAAATCTACGCACTCCCG 528
Db    804 CGCAACACCATGAACTCCGTCGTCGACCCCGCGACGCTCCGCGAGCTCTACCTGCTGCCG 863

Qy    529 TTCCAGATTGCTGTGCGAGACTCCCAGCCGGGTGCGTTCATGACGGCGTACAATGGCATC 588
Db    864 TTCGAGATCGCCGTCGACGAGTCCGACCCGTGGTCCGTCATGGCCGCGTACAACGACGTC 923

Qy    589 AATGGCGTGTCGTGCAGCGAGAACCCTAAATATCTTGATGGGATGCTTCGAAAGGAATGG 648
Db    924 AACGGCGTCCCCGCGACCGAGCACCACCACGTCGTCAACGAGGTCCTCAAGGGCGAGTGG 983

Qy    649 GGTTGGGATGGCCTAATCATGAGCGACTGGTACGGCACATACAGTACCACAGAAGCCGTT 708
Db    984 GGCTACACCGGCCTCGTCATGTCCGACTGGTTCGCGACCCGGACCGCCGCACCCGCCGCC 1043

Qy    709 GTGGCAGGCCTCGACCTCGAGATGCCCGGACCTCCACGCTTCCGAGGAGAAACACTCAAG 768
Db   1044 GCCGGCGGGCTCGACCTCGTCATGCCCGGGCCCGACGGCCCCTGGGGCGACGCGCTCGTC 1103

Qy    769 TTCAACGTCTCCAACGGAAAGCCCTTTATCCACGTCATTGACCAGAGGGCTAGGGAAGTT 828
Db   1104 GCCGCCGTGCGCAGCGGCGAGCTCGACGAGTCCGTCGTCGACGACCACCTGCGCCGCCTG 1163

Qy    829 CTTCAGTTCGTCAAGAAGTGTGCTGCCTCCGGAG---TGACGGAGAACGGCCCCGAGACG 885
Db   1164 CTCGTCCTCGCCGCACGCGTCGGCGCCCTCGGCGACCTGCGGGACTACCCCGACGACCTG 1223

Qy    886 ACTGTCAACAACACCCCCGAAACGGCAGCTCTCCTCCGGAAGGTTGGCAACGAGGGCATC 945
Db   1224 CCCGCCCCCGACAGCGCCGTCCGGCGCGAGCAGCTCACGCGCCTCGCCGCCGCCGGCATG 1283

Qy    946 GTGCTGCTGAAGAACGAGAACAACGTTCTGCCCTTGAGCAAGAAGAAGAAGACGCTGATT 1005
Db   1284 ACCGTCCTCACCAACGCCGACGACACCCTGCCGCTCGCGCGCGGCACCCGCGTCGCACTC 1343

Qy   1006 GTCGGCCCCAACGCCAAGCAGGCCACATACCACGGCGGAGGCTCTGCCGCACTCAGGGCC 1065
Db   1344 GTCGGGCGGCACGCGCTCGAGACGATCGACATGGGCGGCGGCTCCGCGACCGTCAACCCG 1403

Qy   1066 TACTACGCAGTCACTCCCTTTGACGGCCTCAGCAAGCAGCTCGAGACGCCGCCATCGTAC 1125
Db   1404 CCGTACCAGGTGAGCGTCGCCGAGGGCCTCACCGCGCTGCTCGGCGACGCGGTCGACGTC 1463

Qy   1126 ACCGTCGGCGCCTACACCACCGTTCCTCCCATTCTAGGCGAGCAGTGCCTCACGCCCGAC 1185
Db   1464 GTCGACGGCGTCGAGGTCCGCACCCGCCCCGTGCCCGCGCGGCCCGGGTTCGTCGTGGAC 1523

Qy   1186 GGCGCTCCGGGCATGCGCTGGAGGGTCTTCAACGAGCCCCCTGGTACCCCTAACCGCCAG 1245
Db   1524 CCCGACACCGGCCGGCCCGGCCTGCACCTCACGCTCCTCGCCGCCGACGGCACCGTCCTC 1583

Qy   1246 CACATTGACGAGCTCTTCTTCACCAAGACGGACATGCACCTGGTGGACTACTACCACCCC 1305
Db   1584 GACGAGCGGCACGACGCGCCGTCGACCGTCATGGTCGGCTTCGACGACGACTTCCCGCAG 1643

Qy   1306 AAGGCGGCAGACACGTGGTACGCCGACATGGAGGGCACGTACACCGCCGACGAGGACTGC 1365
Db   1644 GCCGTCGCCCGCGTCCGGTTCCGTGCCCGCGTCGCCGGCGAAGGCGCGCTCGAGGTCGGC 1703

Qy   1366 ACCTACGAGCTCGGCC---------TCGTCGTCTGCGGCACGGCAAAGGCGTACGTAGAC 1416
Db   1704 GCGATCGGCGTCGGACGGTGGCAGGTGACCGCAGGCGGCACCGAGCTCGCCTGGACGCTC 1763

Qy   1417 GACCAGCTCGTCGTCGACAACGCCACCAAGCAGGTCCCCGGCGATGCCTTCTTCGGCTCC 1476
Db   1764 GCGACGTCCGGCACCGGGTTCGCCGAGGAGATGCTCGCGCCGCCGACCCGCACCGACCAG 1823

Qy   1477 GCCACCCGCGAG---GAGACGGGCCGCATCAATCTCGTCAAGGGCAACACGTACAAGTTC 1533
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Qy   1534 AAGATCGAGTTCGGCTCCGCACCCACCTACACCCTCAAGGGCGACACCATCGTCCCCGGC 1593
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Db   1944 GCGGGCGTCGGGCTGTTCGGGCTCGTCGCCCGACCCGCCCCGGAGGCGGAGGACGACGTC 2003

Qy   1645 ATCGAAAAGTCCGTCGCCCTCGCCAAGGAGCACGACCAGGTCATCATCTGCGCGGGCCTT 1704

Db   2004 ATCACCCGCGCCGCGGCGGCCGCCGCGCAGGCGGACGTCGCCGTCGTCGTCGTGGGGCTG 2063

Qy   1705 AACGCCGACTGGGAGACCGAGGGCGCCGACCGCGCGAGCATGAAGCTCCCCGGCGTGCTG 1764

Db   2064 ACCGAGGAGGAGGAGACGGAGTCCGTCGACAAGTCCACGATCGCGCTGCCCGGCGCGCAG 2123

Qy   1765 GACCAGCTCATTGCCGACGTGGCCGCCGCGAACCCAAACACCGTCGTCGTCATGCAGACG 1824

Db   2124 GACGCGCTCGTGCGGGCCGTCGCCGCGGCCGCTCGCCGCACGGTCGTCGTGGTCAACGCC 2183

Qy   1825 GGCACCCCCGAGGAGATGCCCTGGCTCGACGCCACGCCCGCCGTCATCCAGGCCTGGTAC 1884

Db   2184 GCGACGCCGGTGCTCATGCCGTGGCTCGACGACGTCGACGCCGTGCTGTGGGCCGGGCTC 2243

Qy   1885 GGCGGCAACGAGACGGGCAACTCCATTGCCGACGTCGTCTTTGGCGACTACAACCCCTCG 1944

Db   2244 CCCGGCCAGGAGGGCGGGCACGCCGTGGCCGCCGCGCTGCTCGGCGACCAGGAGCCGACC 2303

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Qy   2065 GAGTTTGCCGACAAGGACGTCAATTTCCCCTTTGGCCACGGCCTGTCCTACACCACTTTT 2124

Db   2424 GCCGACCGGGCGCCCGCGCCCGCGTTCTGGCTCGGGCACGGCCTCGGGTACGCGACGTGG 2483

Qy   2125 GCCTTTTCCAATCTCTCCGTGTCTCACAAGGACGGCAAGCTGAGCGTGTCCCTCTCCGTG 2184

Db   2484 GAGTACGCCGACGCGACGCTCGACACGGACGGCGACGCCCCCGCGGTGACCGTCACCGTG 2543

Qy   2185 AAGAACACCGGCTCCGTGCCCGGCGCACAGGTGGCCCAGCTCTACGTCAAGCCCCTCCAA 2244

Db   2544 ACCAACACCGGCGCGCGCACCAGCCGCGAGGTCGTCCAGGTCTACCTGGAGCCCGCGTCG 2603

Qy   2245 GCGGCCAAGATTAACCGCCCCGTCAAGGAGCTCAAGGGCTTCGCAAAGGTCGAACTGCAG 2304

Db   2604 TCCGACGAGCCCGTGCGCCTCGTCGGCTGGGCCGACGCGACCGTCGACGCCGGGGCGTCC 2663

Qy   2305 CCCGGCGAGACG 2316

Db   2664 GCCCGCGTCACG 2675


RESULT 8
ATUCBG1
LOCUS       ATUCBG1                 3710 bp    DNA     linear   BCT 26-APR-1993
DEFINITION  A.tumefaciens beta-D-glucosidase (cbg-1) gene, complete cds.
ACCESSION   M59852
VERSION     M59852.1  GI:142221
KEYWORDS    beta-D-glucosidase.
SOURCE      A.tumefaciens DNA.
  ORGANISM  Agrobacterium tumefaciens
            Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
            Rhizobiaceae; Rhizobium.
REFERENCE   1  (bases 1 to 3710)
  AUTHORS   Castle,L.A., Smith,K.D. and Morris,R.O.
  TITLE     Cloning and sequencing of an Agrobacterium tumefaciens
            beta-glucosidase gene involved in modifying a vir-inducing plant
            signal molecule
  JOURNAL   J. Bacteriol. 174 (5), 1478-1486 (1992)
  MEDLINE   92165721
   PUBMED   1537792
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ORIGIN

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  Matches 1195;  Conservative    0;  Mismatches 1171;  Indels   69;  Gaps    8;

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Qy      77 ACTTCTGGCACACAAAGGCTCTCCCCAAGCATGGAGTCCCCTCTCTCCGCTTTACAGATG 136

Db     245 ATTTCTGGACGACCGTCGCGATCGAGCGGCTCGGCGTGCCGAAGATCAAGGTTACCGACG 304

Qy     137 GCCCCAACGGCGTAAGAGGGACCAAGT---TCTTCAATGGCGTCCCTGCGGCCTGCTTCC 193

Db     305 GCCCCAATGGCGCACGCGGCGGCGGGTCGCTGGTCGGCGGCGTCAAGTCCGCCTGCTTCC 364

Qy     194 CTTGCGGCACGTCGCTCGGTTCCACATTCAACCAAACTCTGCTCGAAGAGGCAGGTAAGA 253

Db     365 CGGTGGCAATCGCGCTTGGAGCGACGTGGGACCCGGAGCTCATCGAGCGCGCCGGCGTGG 424

Qy     254 TGATGGGCAAAGAGGCCATCGCTAAGAGTGCGCATGTGATCCTCGGCCCGACTATCAACA 313

Db     425 CGCTGGGAGGACAAGCCAAGAGCAAGGGCGCGTCGGTGCTTCTGGCGCCGACCGTCAACA 484

Qy     314 TGCAACGCTCCCCTCTCGGTGGACGTGGCTTCGAGTCGATTGGTGAGGATCCGTTCCTGG 373

Db     485 TTCACCGCTCCGGCCTCAATGGCCGCAACTTCGAATGCTATTCGGAAGACCCGGCGCTGA 544

Qy     374 CGGGCTTGGGAGCTGCGGCTCTCATCCGCGGCATTCAGAGCACTGGAGTGCAGGCTACGA 433

Db     545 CCGCCGCCTGCGCCGTCGCCTATATCAATGGCGTGCAGAGCCAGGGTGTGGCCGCCACGA 604
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Qy    434 TCAAGCACTTTTTGTGCAATGATCAGGAGGACAGGCGCATGATGGTGCAGAGCATCGTCA 493
Db    605 TCAAGCACTTCGTCGCCAACGAGTCCGAGATCGAGCGGCAGACCATGTCCTCCGATGTCG 664

Qy    494 CGGAGCGGGCTCTCCGTGAAATCTACGCACTCCCGTTCCAGATTGCTGTGCGAGACTCCC 553
Db    665 ATGAGCGGACGCTGCGCGAAATCTATCTGCCGCCTTTCGAGGAGGCGGTGAAGAAGGCCG 724

Qy    554 AGCCGGGTGCGTTCATGACGGCGTACAATGGCATCAATGGCGTGTCGTGCAGCGAGAACC 613
Db    725 GCGTGAAGGCCGTCATGTCCTCCTACAACAAGCTCAACGGCACCTATACGAGCGAAAATC 784

Qy    614 CTAAATATCTTGATGGGATGCTTCGAAAGGAATGGGGTTGGGATGGCCTAATCATGAGCG 673
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Qy    674 ACTGGTACGGCACATACAGTACCACAGAAGCCGTTGTGGCAGGCCTCGACCTCGAGATGC 733
Db    845 ACTGGTTCGGCTCGCACTCGACGGCTGAAACCATCAATGCCGGGCTCGATCTGGAGATGC 904

Qy    734 CCGGACCTCCACGCTTCCGAGGAGAAACACTCAAGTTCAACGTCTCCAACGGAAAGCCCT 793
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Qy    794 TTATCCACGTCATTGACCAGAGGGCTAGGGAAGTTCTTCAGTTCGTCAAGAAGTGTGCTG 853
Db    965 AGGCCGAGACCGTGCGCGCTTCGGCACGGCGTATTCTCCTTCTGCTCGAACGCGTCGGCG 1024

Qy    854 CCTCCGGAGTGACGGAGAACGGCCCCGAGACGACTGTCAACAACACCCCCGAAACGGCAG 913
Db   1025 CCTTTGAAAAGGCGCCTGATCTCGCCGAACACGCGCTTGATCTGCCGGAAGATCGTGCGC 1084

Qy    914 CTCTCCTCCGGAAGGTTGGCAACGAGGGCATCGTGCTGCTGAAGAACGAGAACAACGTTC 973
Db   1085 TCATCCGCCAACTCGGTGCGGAGGGTGCTGTACTCCTGAAGAATGACGGAGTGCTGCCGC 1144

Qy    974 TGCCCTTGAGCAAGAAGAAGAAGACGCTGATTGTCGGCCCCAACGCCAAGCAGGCCACAT 1033
Db   1145 TTGCCAAGTCGTCCTTCGACCAGATCGCCGTCATCGGCCCCAATGCGGCTTCCGCACGCG 1204

Qy   1034 ACCACGGCGGAGGCTCTGCCGCACTCAGGGCCTACTACGCAGTCACTCCCTTTGACGGCC 1093
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Qy   1094 TCAGCAAGCAGCTCGAGACGCCGCCATCGTACACCGTCGGCGCCTACACCACCGTTCCTC 1153
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Qy   1214 TCAACGAGCCCCCTGGTACCCCTAACCGCCAGCACATTGACGAGCTCTTCTTCACCAAGA 1273
Db   1364 ACTTCAAGGGACGCGGCTTCGAGAGCCGTCCGGTCCATGTCGAGACCGTCGAAAAGGGCG 1423

Qy   1274 CGGACATGCACCTGGTGGACTACTACCACCCCAAGGCGGCAGACACGTGGTACGCCGACA 1333
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Qy   1334 TGGAGGGCACGTACACCGCCGACGAGGACTGCACCTACGAGCTCGGCCTCGTCGTCTGCG 1393
Db   1484 TGACGGCGACCTTCGTGCCGCAGGAAACCGGTGAACACATCTTCGGCATGACCAATGCTG 1543

Qy   1394 GCACGGCAAAGGCGTACGTAGACGACCAGCTCGTCGTCGACAACGCCACCAAGCAGGTCC 1453
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Qy   1454 CCGGCGATGCCTTCTTCGGCTCCGCCACCCGCGAGGAGACGGGCCGCATCAATCTCGTCA 1513
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Qy   1754 CCGGCGTGCTGGACCAGCTCATTGCCGACGTGGCCGCCGCGAACCCAAACACCGTCGTCG 1813
Db   1886 CGGGTCGCCAGGAGGAGCTGATCGAGGCGGTCGCCGAAACCAATCCCAACGTGGTCGTGG 1945

Qy   1814 TCATGCAGACGGGCACCCCCGAGGAGATGCCCTGGCTCGACGCCACGCCCGCCGTCATCC 1873
Db   1946 TACTGCAAACGGGTGGTCCCATCGAGATGCCATGGCTCGGCAAGGTGCGTGCGGTGCTGC 2005

Qy   1874 AGGCCTGGTACGGCGGCAACGAGACGGGCAACTCCATTGCCGACGTCGTCTTTGGCGACT 1933
Db   2006 AGATGTGGTATCCCGGCCAGGAACTTGGCAATGCGCTTGCGGACGTTCTCTTTGGTGATG 2065

Qy   1934 ACAACCCCTCGGGCAAGCTGTCCCTCAGCTTCCCCAAGCGCCTGCAGGACAACCCCGCGT 1993
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Qy   2042 TCTACGTCGGGTACAGGTACTACGAGTTTGCCGACAAGGACGTCAATTTCCCCTTTGGCC 2101
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Qy   2393 AAAAGGGTGACTATGAGGTTATCGTGAGCGACAGC 2427
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RESULT 9
ABI293760
LOCUS ABI293760 2636 bp mRNA linear PLN 09-AUG-2000
DEFINITION Agaricus bisporus mRNA for putative beta glucosidase (bg1 gene), strain D649.
ACCESSION AJ293760
VERSION AJ293760.1 GI:9796011
KEYWORDS beta glucosidase; bg1 gene.
SOURCE Agaricus bisporus.

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            Agaricales; Agaricaceae; Agaricus.
REFERENCE   1  (bases 1 to 2636)
  AUTHORS   Morales-Almora,P. and Thurston,C.F.
  TITLE     Molecular analysis of the cellulolytic genes in Agaricus bisporus
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2636)
  AUTHORS   Morales-Almora,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) Morales-Almora P., Microbiology, King's
            College London, 150 Stamford Street, London, SE1 8WA, UNITED
            KINGDOM
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BASE COUNT      657 a    603 c    682 g    694 t
ORIGIN

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Qy      62 TGCTGGCTGGTATCGACTTCTGGCACACAAAGGCTCTCCCCAAGCATGGAGTCCCCTCTC 121
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Qy     122 TCCGCTTTACAGATGGCCCCAACGGCGTAAGAGGGACCAAGTTCTTCAATGGCGTCCCTG 181
Db     161 TGAAGGTTAGCGACGGGCCCAATGGTATCCGAGGAAATCATTTCTTTATGGGCACGCCAG 220

Qy     182 CGGCCTGCTTCCCTTGCGGCACGTCGCTCGGTTCCACATTCAACCAAACTCTGCTCGAAG 241
Db     221 CCAAGTGTTTGCCGTCATCCACTGCAATGGGCGCAACTTTCGATCGTGACCTACTTGAAG 280

Qy     242 AGGCAGGT---AAGATGATGGGCAAAGAGGCCATCGCTAAGAGTGCGCATGTGATCCTCG 298
Db     281 AAGTTGGTCTCAAGCTTCTCGCTAGAGAAGCAAAGCTCAGATCCGCCTCTGTTATCCTCG 340

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Db     341 CTCCAACTTGTAACATCCAACGTAATCCCCTCGGTGGTAGGAGTTTTGAAAGTTTTTCGG 400

Qy     359 AGGATCCGTTCCTGGCGGGCTTGGGAGCTGCGGCTCTCATCCGCGGCATTCAGAGCACTG 418
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Qy     419 GAGTGCAGGCTACGATCAAGCACTTTTTGTGCAATGATCAGGAGGACAGGCGCA-TGATG 477
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Qy     478 GTGCAGAGCATCGTCACGGAGCGGGCTCTCCGTGAAATCTACGCACTCCCGTTCCAGATT 537
Db     521 ATGACAGTATTCATTACCGAACGACCTCTTCGGGAGATTTATCTCCTTCCGTTCATGCTG 580

Qy     538 GCTGTGCGAGACTCCCAGCC--GGGTGCGTTCATGACGGCGTACAATGGCATCAATGGCG 595
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Qy     656 ATGGCCTAATCATGAGCGACTGGTACGGCACATACAGTACCACAGAAGCCGTTGTGGCAG 715
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Qy     716 GCCTCGACCTCGAGATGCCCGGACCTCCACGCTTCCG---AGGAGAAACACTCAAGTTCA 772
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Qy     773 ACGTCTCCAACGGAAAGCCCTTTATCCACGTCATTGACCAGAGGGCTAGGGAAGTTCTTC 832
Db     821 CAATTCAATCTAGGAAAGTAACCGCCAAGAAAGTCAAAGAGCGTGCTCGAAAAGTCCTCG 880

Qy     833 AGTTCGTCAAGAAGTGTGCT------GCCTCCGGAGTGACGGAGAACGGCCCCGAGACGA 886
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Qy     887 CTGTCAACAACACCCCCGAAACGGCAGCTCTCCTCCGGAAGGTTGGCAACGAGGGCATCG 946
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Db    1001 TTCTGCTCAAGAACGACAAGAAAGTCCTTCCCTTGGACCGTAAGAGTTTAAAGAAAGTTG 1060

Qy    1001 TGATTGTCGGCCCCAACGCCAAGCAGGCCACATACCACGGCGGAGGCTCTGCCGCACTCA 1060
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Qy    1215 CAACGAGCC----CCCTGGTACCCCTAACCGCCAGCACATTGACGAGCTCTTCTTCACCA 1270
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Qy    1271 AGACGGACATGCACCTGGTGGACTACTACCACCCCAAGGCGGCAGACACGTGGTACGCCG 1330
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Qy    1331 ACATGGAGGGCACGTACACCGCCGACGAG-GACTGCACCTACGAGCTCGGCCTCGTCGTC 1389
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Db   1600 AAAGCCGGTGTCAAGCATGAGATTTATGTCGACTTCTGTAATGTTCGTGGGCCAGCTGAT 1659

Qy   1564 ACCCTCAAGGGCGACACCATCGTCCCCGGCCACGGCTCCCTCCGCGTCGGCGGCTGCAAG 1623

Db   1660 GGTGATGAAACCGAAACAATCATGGATAGTAACCCTGGTATTCGCCTTGGGGGCGCTGAA 1719

Qy   1624 GTCATTGACGACCAGGCCGAAATCGAAAAGTCCGTCGCCCTCGCCAAGGAGCACGACCAG 1683

Db   1720 GTTGAAGATCCTGATGAGCTCCTCAATTCCGCTGTCTCAATCGCAAAAGACGCTGATGCC 1779

Qy   1684 GTCATCATCTGCGCGGGCCTTAACGCCGACTGGGAGACCGAGGGCGCCGACCGCGCGAGC 1743

Db   1780 GTTATTATCGTTGTCGGTTTAAACGGTGATTGGGAGACAGAGGGTAATGACCGTACCACC 1839

Qy   1744 ATGAAGCTCCCCGGCGTGCTGGACCAGCTCATTGCCGACGTGGCCGCCGCGAACCCAAAC 1803

Db   1840 CTTGCCCTTCCCGGCCGTACCGACGAATTGGTACAAAAAGTCGTTGCTGCAAATCCTCGT 1899

Qy   1804 ACCGTCGTCGTCATGCAGACGGGCACCCCCGAGGAGATGCCCTGGCTCGACGCCACGCCC 1863

Db   1900 GCTGTCGTCGTCACTCAAGCGGGTTCCGCTATAACTATGCCTTGGGTCGACCAAGTTTCT 1959

Qy   1864 GCCGTCATCCAGGCCTGGTACGGCGGCAACGAGACGGGCAACTCCATTGCCGACGTCGTC 1923

Db   1960 TCCCTCCTACATACCTGGTATCTAGGTAATGCTACTGGCGATGCTATCGCCGACGTCATT 2019

Qy   1924 TTTGGCGACTACAACCCCTCGGGCAAGCTGTCCCTCAGCTTCCCCAAGCGCCTGCAGGAC 1983

Db   2020 TTTGGGAATCATAATCCTTCTGGAAAGCTTTCATTGACCTTCCCGAAGCGATTGGAGGAT 2079

Qy   1984 AACCCCGCGTTTCTCAACTTCCGCACCGAGGCCGGGCGCACGCTGTACGGCGAGGACGTC 2043

Db   2080 GTTCCTGCTCATGGCTATTTCCATTCTGAGAAAGGAAAGGTGACGTACGCTGAAGGTCTT 2139

Qy   2044 TACGTCGGGTACAGGTACTACGAGTTTGCCGACAAGGACGTCAATTTCCCCTTTGGCCAC 2103

Db   2140 TACGTGGGTTATAAACATTATCAACATCGTAATATCGAACCTCTCTTCGCGTTTGGCCAT 2199

Qy   2104 GGCCTGTCCTACACCACTTTTGCCTTTTCCAATCTCTCCGTGTCTCA 2150

Db   2200 GGTTTATCGTACACGTCGTTCAATATTTCAGACCTTCGTCTCTCACA 2246


RESULT 10
REU80928_2/c
WPCOMMENT
  Sequence split into 4 fragments  LOCUS REU80928 Accession U80928
     Fragment Name      Begin     End
     REU80928_0             1    110000
     REU80928_1        100001    210000
     REU80928_2        200001    310000
     REU80928_3        300001    371255
Continuation (3 of 4) of REU80928 from base 200001 (U80928 Rhizobium etli strain CFN42 s

  Query Match            10.8%;  Score 270;  DB 1;  Length 110000;
  Best Local Similarity  48.0%;  Pred. No. 4.5e-24;
  Matches 1116;  Conservative    0;  Mismatches 1135;  Indels   75;  Gaps    9;

Qy     10 ATTGATGTTGAGGCCATCTTGAAGAAGCTCACCCTGGCCGAGAAGGTCGATCTGCTGGCT 69

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Qy     70 GGTATCGACTTCTGGCACACAAAGGCTCTCCCCAAGCATGGAGTCCCCTCTCTCCGCTTT 129

Db   81089 GGCGATACGTTCTGGTCTTTACCGCCCATCGACCGCCTAGGGATAGGGAGATTGCGCTTG 81030

Qy    130 ACAGATGGCCCCAACGGCGTAAGAGGGACCAAGTTCT---TCAATGGCGTCCCTGCGGCC 186

Db   81029 ACCGACGGCCCCAACGGCGCCCGCGGGGCGGGGTCTTTTGTCGGAGGTGTGACTGCAGCG 80970

Qy    187 TGCTTCCCTTGCGGCACGTCGCTCGGTTCCACATTCAACCAAACTCTGCTCGAAGAGGCA 246

Db   80969 GCTTTCCCGGTGGGCATCGCCATCGGAGCGAGTTGGAACCCGGATCTAGCCAAGGAAATC 80910

Qy    247 GGTAAGATGATGGGCAAAGAGGCCATCGCTAAGAGTGCGCATGTGATCCTCGGCCCGACT 306

Db   80909 GGCAGTGCCCTAGGTGACGAGGTTCTTTCAAAAGGTGCCCACGTCTCGTTAGCCCCCACC 80850

Qy    307 ATCAACATGCAACGCTCCCCTCTCGGTGGACGTGGCTTCGAGTCGATTGGTGAGGATCCG 366

Db   80849 GTTAACATCCAGCGTAGCGTCACAAACGGCCGCAACTTTGAGTGCTTCTCTGAGGATCCG 80790

Qy    367 TTCCTGGCGGGCTTGGGAGCTGCGGCTCTCATCCGCGGCATTCAGAGCACTGGAGTGCAG 426

Db   80789 ATCCTGACGGCGGAACTTGCAGTCGGCTATATCGAAGGTCTGCAGTCCACGAAAGTCGGT 80730

Qy    427 GCTACGATCAAGCACTTTTTGTGCAATGATCAGGAGGACAGGCGCATGATGGTGCAGAGC 486

Db   80729 GCCACGATAAAACATTTCGTCGGCAACGAGTCCGAGATTGAACGTACAACCATCTCTTCA 80670

Qy    487 ATCGTCACGGAGCGGGCTCTCCGTGAAATCTACGCACTCCCGTTCCAGATTGCTGTGCGA 546

Db   80669 GATATCGATGAACGCACGCTGCGCGAAGTCTACCTGATACCCTTTGAGACGGCGGTGAAG 80610

Qy    547 GACTCCCAGCCGGGTGCGTTCATGACGGCGTACAATGGCATCAATGGCGTGTCGTGCAGC 606

Db   80609 CGGGCAAAGGTCTGGGCCGTGATGTCTTCGTATAACAAGCTAAACGGTACTTACACGGCG 80550

Qy    607 GAGAACCCTAAATATCTTGATGGGATGCTTCGAAAGGAATGGGGTTGGGATGGCCTAATC 666

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Qy    667 ATGAGCGACTGGTACGGCACATACAGTACCACAGAAGCCGTTGTGGCAGGCCTCGACCTC 726

Db   80489 ATGTCGGACTGGTTCGGCTCGCGTTCGACCGCACCCACCGTGAATGCCGGGCTGGATCTG 80430

Qy    727 GAGATGCCCGGACCTCCACGCTTCCGAGGAGAAACACTCAAGTTCAACGTCTCCAACGGA 786

Db   80429 GAGATGCCGGGCCCGACTCGCGATCGCGGCTCCAAGCTACTGGCTGCGGTCGAAGGCGGC 80370

Qy    787 AAGCCCTTTATCCACGTCATTGACCAGAGGGCTAGGGAAGTTCTTCAGTTCGTCAAGAAG 846

Db   80369 GAGGTTAGTGTCGAGACGATCCGCGCCTGTGTGCGCAATATCCTGACTTTGATGGAACGC 80310

Qy    847 TGTGCTGCCTCCGGAGTGACGGAGAACGGCCCCGAGACGACTGTCAACAACACCCCCGAA 906

Db   80309 ACCGGCGCTATCAACGATCATCGCGAGTTTAAGGAGTACGCCATTGATCAACCGAAACAT 80250

Qy    907 ACGGCAGCTCTCCTCCGGAAGGTTGGCAACGAGGGCATCGTGCTGCTGAAGAACGAGAAC 966

Db   80249 AGGGCATTGATCAGGCGCGCGGGAGCGGAAAGCGCAGTTCTGCTACAGAATGACGGGATC 80190

Qy    967 AACGTTCTGCCCTTGAGCAAGAAGAAGAAGACGCTGATTGTCGGCCCCAACGCCAAGCAG 1026

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Qy   1027 GCCACATACCACGGCGGAGGCTCTGCCGCACTCAGGGCCTACTACGCAGTCACTCCCTTT 1086

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Qy   1087 GACGGCCTCAGCAAGCAGCTCGAGACGCCGCCATCGTACACCGTCGGCGCCTACACCACC 1146

Db   80075 CAGGGGCTGGTGGACGCGCTGGGTGAGGAGAATCTGTGCTACGCTCAGGGCTGCAACAAT 80016
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Qy   1207 AGGGTCTTCAACGAGCCCCCTGGTACCCCTAACCGCCAGCACATTGACGAGCTCTTCTTC 1266
Db  79962 AAGGGAGCTAGCTGGCGAACCGGT-----------GAAGGTCGTCGAGGAACCGTCGAGC 79914

Qy   1267 ACCAAGACGGACATGCACCTGGTGGACTACTACCACCCCAAGGCGGCAGACACGTGGTAC 1326
Db  79913 CTTGGTGTATGGTTGCCCCCCGTGGCCGAGGGCTTTGTCGATCCCCTTCGC---TTTTCG 79857

Qy   1327 GCCGACATGGAGGGCACGTACACCGCCGACGAGGACTGCACCTACGAGCTCGGCCTCGTC 1386
Db  79856 GCTAGAATGCGCACCATCTTCACAGCCTCGGAAGCCGGCGTCTATCGCGTCGGACTAACC 79797

Qy   1387 GTCTGCGGCACGGCAAAGGCGTACGTAGACGACCAGCTCGTCGTCGACAACGCCACCAAG 1446
Db  79796 TCGGCCGGGCTTGGCCGGGTCTATGTGGACGGCAGACTTGTGGTGGACGCTTGGGCTTCC 79737

Qy   1447 CAGGTCCCCGGCGATGCCTTCTTCGGCTCCGCCACCCGCGAGGAGACGGGCCGCATCAAT 1506
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Qy   1507 CTCGTCAAGGGCAACACGTACAAGTTCAAGATCGAGTTCGGCTCCGCACCCACCTACACC 1566
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Qy   1567 CTCAAGGGCGACACCATCGTCCCCGGCCACGGCTCCCTCCGCGTCGGCGGCTGCAAGGTC 1626
Db  79616 CTCTATATCGCCGCAATTCGGGTAGGAATAGGC----------------------AGA 79581

Qy   1627 ATTGACGACCAGGCCGAAATCGAAAAGTCCGTCGCCCTCGCCAAGGAGCACGACCAGGTC 1686
Db  79580 TTTTCGGCCGAAGCGGAGATTGCCGAGGCAGCAGCCGTCGCGGCAAAGGCTGATCATGCG 79521

Qy   1687 ATCATCTGCGCGGGCCTTAACGCCGACTGGGAGACCGAGGGCGCCGACCGCGCGAGCATG 1746
Db  79520 GTAGTCTTCGTGGGCAGAACGGGCGACTGGGATACCGAGGGCTCCGATCTTCGCGGTATT 79461

Qy   1747 AAGCTCCCCGGCGTGCTGGACCAGCTCATTGCCGACGTGGCCGCCGCGAACCCAAACACC 1806
Db  79460 GCACTTCCCGGTCTGCAGAACCAGCTTGTTGAGGCGGTAATTGCGGCCAATCCGAACACG 79401

Qy   1807 GTCGTCGTCATGCAGACGGGCACCCCCGAGGAGATGCCCTGGCTCGACGCCACGCCCGCC 1866
Db  79400 ATCGTCGTACTACAAACCGGTGGACCGGTGGAAATGCCCTGGCTTTCCGGTGCTCGTGCA 79341

Qy   1867 GTCATCCAGGCCTGGTACGGCGGCAACGAGACGGGCAACTCCATTGCCGACGTCGTCTTT 1926
Db  79340 GTACTGCAATGCTGGTATCCCGGACAGGAGGCTGGCAACGCGATCGCCGATGTGCTCCTC 79281

Qy   1927 GGCGACTACAACCCCTCGGGCAAGCTGTCCCTCAGCTTCCCCAAGCGCCTGCAGGACAAC 1986
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Qy   1987 CCCGCGTTTCTCAACTTCCGCACCG----------AGGCCGGGCGCACGCTGTACGGC 2034
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Qy   2035 GAGGACGTCTACGTCGGGTACAGGTACTACGAGTTTGCCGACAAGGACGTCAATTTCCCC 2094
Db  79160 GAAGGTGTGTTCGTCGGTTATCGGCACTACGACCGCCACGGCATTAAGCCGCTGTTCCCG 79101

Qy   2095 TTTGGCCACGGCCTGTCCTACACCACTTTTGCCTTTTCCAATCTCTCCG------TGTCT 2148
Db  79100 TTCGGTCATGGTCTCGGTTATTCAAGCTTTGCGATGTCGGACCTGACGGTAGGGCTACCA 79041

Qy   2149 CACAAGGACGGCAAGCTGAGCGTGTCCCTCTCCGTGAAGAACACCGGCTCCGTGCCCGGC 2208
Db  79040 GACGCTGCCGGCGCGGTGACAGTGACACTGGAATTGACCAACATCAGCGAGCGGCCAGGT 78981

Qy   2209 GCACAGGTGGCCCAGCTCTACGTCAAGCCCCTCCAAGCGGCCAAGATTAACCGCCCCGTC 2268
Db  78980 TCGGCAGTGGTGCAAATCTATGTCGGCGATGTTGAAGCATC---TATACCCAGACCGGTT 78924

Qy   2269 AAGGAGCTCAAGGGCTTCGCAAAGGTCGAACTGCAGCCCGGCGAGA 2314
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RESULT 11
AX489445
LOCUS AX489445 2601 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 6745 from Patent WO02053728.
ACCESSION AX489445
VERSION AX489445.1 GI:22323457
KEYWORDS .
SOURCE Candida albicans.
ORGANISM Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE 1
AUTHORS Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 6745 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1. .2601
/organism="Candida albicans"
/db_xref="taxon:5476"
BASE COUNT 917 a 334 c 484 g 866 t
ORIGIN

Query Match 8.2%; Score 205; DB 6; Length 2601;
Best Local Similarity 46.7%; Pred. No. 7.6e-16;
Matches 1031; Conservative 0; Mismatches 1097; Indels 78; Gaps 9;

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Db      14 TTGATATTGATAATATATTATCTCAATTGACATTAGAAGAAAAAATTGGATTAGTAGGTG 73

Qy      71 GTATCGACTTCTGGCACACAAAGGCTCTCCCCAAGCATGGAGTCCCCTCTCTCCGCTTTA 130
Db      74 GAATTGATTTTTGGCATACATATCCAATTTCTCGATTAAACATTCCCAAAGTGAGATTCA 133

Qy     131 CAGATGGCCCCAACGGCGTAAGAGGGACCAAGTTCTTCAATGGCGTCCCTGCGGCCTGCT 190
Db     134 CTGATGGTCCCAATGGTATTAGAGGCACAAGGTTTTTCAATGGTGTTCCTCTGGCTTGTT 193

Qy     191 TCCCTTGCGGCACGTCGCTCGGTTCCACATTCAACCAAACTCTGCTCGAAGAGGCAGGTA 250
Db     194 TCCCCTGTGGAACTGGATTAGCTGCTACTTTTGATCATGAATTATTATTGACAACCGGGA 253

Qy     251 AGATGATGGGCAAAGAGGCCATCGCTAAGAGTGCGCATGTGATCCTCGGCCCGACTATCA 310
Db     254 AATTAATGAACATTGAAGCTAAATTTAAAAATGCGCACGTGATCTTGGGTCCTACGATGA 313

Qy     311 ACATGCAACGCTCCCCTCTCGGTGGACGTGGCTTCGAGTCGATTGGTGAGGATCCGTTCC 370
Db     314 ATATTCAACGAGGCCCATTAGGTGGCCGAGGATTTGAATCATTTTCTGAAGATCCTTATT 373

Qy     371 TGGCGGGCTTGGGAGCTGCGGCTCTCATCCGCGGCATTCAGAGC---ACTGGAGTGCAGG 427
Db     374 TAACTGGACAAATTGCCAGTGCTATAATTAAGGGTATTCAATATGATAATGAAATTGGTG 433

Qy     428 CTACGATCAAGCACTTTTTGTGCAATGATCAGGAGGACAGGCGCATGATGGTGCAGAGCA 487
Db     434 CCACGGTTAAACATTATGTTTGTAATGATTTAGAAGATGAAAGGAGTGCTAGTGATTCTT 493

Qy     488 TCGTCACGGAGCGGGCTCTCCGTGAAATCTACGCACTCCCGTTCCAGATTGCTGTGCGAG 547
Db     494 TGGTTACACCAAGAGCATTGAGAGAAATTTATTTAGAACCATTTAGAATAGCTATTAAAG 553

Qy     548 ACTCCCAGCCGGGTGCGTTCATGACGGCGTACAATGGCATCAATGGCGTGTCGTGCAGCG 607
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Db    554 AAAGTAATCCAATTTGTTTGATGACAGGGTATAATAAAGTTAATGGTGAACATGTTTCTC 613

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Qy   1001 TGATTGTCGGCCCCAACGCCAAGCAGGCCACATACCACGGCGGAGGCTCTGCCGCACTCA 1060

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Qy   1853 ACGCCACGCCCGCCGTCATCCAGGCCTGGTACGGCGGCAACGAGACGGGCAACTCCATTG 1912

Db   1934 ATAAACTGAAAGCTTTGTTGCATTGTTGGTATGGTGGGAATGAAAGTGGGAATGCCATTG 1993

Qy   1913 CCGACGTCGTCTTTGGCGACTACAACCCCTCGGGCAAGCTGTCCCTCAGCTTCCCCAAGC 1972

Db   1994 CTGATATTTTATTTGGTAATGTCAATCCTAATGGGAAATTATCATTGACTTTCCCATTGA 2053

Qy   1973 GCCTGCAGGACAACCCCGCGTTTCTCAACTTCCGCACCGAGGCCGGGCGCACGCTGTACG 2032

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RESULT 12
SC8A6

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LOCUS       SC8A6                37445 bp    DNA     linear   BCT 12-MAY-2002
DEFINITION  Streptomyces coelicolor cosmid 8A6.
ACCESSION   AL031013 AL645882
VERSION     AL031013.2  GI:20520810
KEYWORDS    beta-glucosidase; elongation factor G; fusA; sucC; succinyl-coa
            synthetase alpha chain; succinyl-coa synthetase beta chain; sucD;
            TPP-requiring enzyme; transfer-RNA-Leu; TTA Leu codon.
SOURCE      Streptomyces coelicolor A3(2).
  ORGANISM  Streptomyces coelicolor A3(2)
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE   1  (bases 1 to 37445)
  AUTHORS   Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
            Kinashi,H. and Hopwood,D.A.
  TITLE     A set of ordered cosmids and a detailed genetic and physical map
            for the 8 Mb Streptomyces coelicolor A3(2) chromosome
  JOURNAL   Mol. Microbiol. 21 (1), 77-96 (1996)
  MEDLINE   97000351
   PUBMED   8843436
REFERENCE   2  (bases 1 to 37445)
  AUTHORS   Seeger,K.J. and Harris,D.
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 37445)
  AUTHORS   Parkhill,J., Barrell,B.G. and Rajandream,M.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-1998) Streptomyces coelicolor sequencing project,
            Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
            CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
            David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
            Colney, Norwich, Norfolk NR4 7UH, UK
COMMENT     On May 9, 2002 this sequence version replaced gi:3288600.
            Notes:
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Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC.
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary strand).
The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database.
The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 8A6 lies between 3F9 and 1F2 on the AseI-A genomic restriction fragment.

FEATURES Location/Qualifiers

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/organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
/db_xref="taxon:100226"
/clone="cosmid 8A6"

misc_feature 2. .107
/note="nominal overlap with St8A6 from 1 to 106
nominal overlap with cosmid 3F9 from 19725 to 19830"

stem_loop 657. .711
/note="hairpin loop with 23 bp stem"

gene complement(730. .2160)
/gene="SCO6581"

CDS complement(730. .2160)
/gene="SCO6581"
/note="SC8A6.02c, probable transmembrane transport protein, len: 476 aa; some similarity to e.g. TR:Q51330 (EMBL:U4007 5) oxalate:formate antiport protein from Oxalobacter formig enes (418 aa), fasta scores; opt: 226 z-score: 230.1 E(): 1 .4e-05, 24.1% identity in 436 aa overlap"
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CDS complement(5626. .7308)
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Qy         94 GCTCTCCCCAAGCATGGAGTCCCCTCTCTCCGCTTTACAGATGGCCCCAACGGCGTAAGA 153
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Qy        154 GGGACCAAGTTCTTCAATGGCGTCCCTGCGGCCTGCTTCCCTTGCGGCACGTCGCTCGGT 213
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Qy        334 GGACGTGGCTTCGAGTCGATTGGTGAGGATCCGTTCCTGGCGGGCTTGGGAGCTGCGGCT 393
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Qy        454 GATCAGGAGGACAGGCGCATGATGGTGCAGAGCATCGTCACGGAGCGGGCTCTCCGTGAA 513
Db      28031 GACTCCGAGACCGACCGCCTCACCGTCGACGTGCGGGTGGGCGAACGGGCGCTGCGAGAG 28090

Qy        514 ATCTACGCACTCCCGTTCCAGATTGCTGTGCGAGACTCCCAGCCGGGTGCGTTCATGACG 573
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Qy       1078 --ACTCCCTTTGACGGCCTCAGCAAGCAGCTCG-AGACGCCGCCATCGTACACCGTCGGC 1134
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Qy       1195 GGCATGCGCTGGAGGGTCTTCAACGAGCCC--CCTGGTACCCCTAACCGCCAGCACATTG 1252
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Qy       1313 CAGACACGTGGTACG--CCGACATGGAGGGCACGTACACCGCCGACGAGGACTGCACCTA 1370
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Qy       1371 CGAGCTCGGCCTCGTCGTCTGCGGCACGGCAAAGGCGTACGTAGACGACCAGCTCGTCGT 1430
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Qy       1569 CAAGGGCGACA-----------CCATCGTCCCCGGCCACGGCTCCCTCCGCGTCGGCGG 1616
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Qy   1857 CACGCCCGCCGTCATCCAGGCCTGGTACGGCGGCAACGAGACGGGCAACTCCATTGCCGA 1916
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Qy   2097 TGGCCACGGCCTGTCCTACACCACTT---------TTGCCTTTTCCAATCTCTCCGTGTC 2147
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Qy   2208 CGCACAGGTGGCCCAGCTCTACGTCAAGCCCCTCCAAGCGGCCAAGATTAACCGCCCCGT 2267
Db  29881 CCGGGAGGTCGTCCAGGTGTACCT---GGCCCGGCCCGCGTCGGCCCTCGACCGTCCCGC 29937

Qy   2268 CAAGGAGCTCAAGGGCTTCGCAAAGGTCGAACTGCAGCCCGGCGAGACGAAGGCGGTGAC 2327
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Qy   2328 AATCGAGGAGCAGGAGAAGTACGTCGCTGCGTATTTTGATGAGGAGC 2374
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SOURCE      Unknown.
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REFERENCE   1  (bases 1 to 3241)
  AUTHORS   Betlach,M.C. and McDaniel,R.
  TITLE     Nucleic acids encoding narbonolide polyketide synthase enzymes from
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  JOURNAL   Patent: US 6303767-A 11 16-OCT-2001;
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Db   1211 ACGGACGCGCGCTGGGCCAGGACATGGTTCTGGGCCCGATGATGAACAACATCCGGGTGC 1270

Qy    326 CTCTCGGTGGACGTGGCTTCGAGTCGATTGGTGAGGATCCGTTCCTGGCGGGCTTGGGAG 385
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Qy    386 CTGCGGCTCTCATCCGCGGCATTCAGAGCACTGGAGTGCAGGCTACGATCAAGCACTTTT 445
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Qy    446 TGTGCAATGATCAGGAGGACAGGCGCATGATGGTGCAGAGCATCGTCACGGAGCGGGCTC 505
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Qy    566 TCATGACGGCGTACAATGGCATCAATGGCGTGTCGTGCAGCGAGAACCCTAAATATCTTG 625
Db   1508 TCATGTGTGCCTATAACGGCGTCAACGGCAAGCCGTCCTGCGGCAACGACGAGCTGCTCA 1567

Qy    626 ATGGGATGCTTCGAAAGGAATGGGGTTGGGATGGCCTAATCATGAGCGACTGGTACGGCA 685
Db   1568 ACAACGTGCTGCGCACGCAGTGGGGCTTCCAGGGCTGGGTGATGTCCGACTGGCTCGCCA 1627

Qy    686 CATACAGTACCACAGAAGCCGTTGTGGCAGGCCTCGACCTCGAGATGCCCGGACCTCCAC 745
Db   1628 C---CCCGGGCACGGACGCCATCACCAAGGGCCTCGACCAGGAGAT----GGGCGTCGAG 1680

Qy    746 GCTTCCGAGGAGAAACACTCAAGTTCAACGTCTCCAACGGAAAGCCCTTTATCCACGTCA 805
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Qy    806 TTGACCAGAGGGCTAGGGAAGTTCTTCAGTTCGTCAAGAAGTGTGCTGCCTCCGGAGTGA 865
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Qy    866 CGGAGAACGGCCCCGAGACGACTGTCAACAACACCCCCGAAACGGCAGCTCTCCTCCGGA 925
Db   1781 CCGTGACGCGGTCGGCGGAGCGCATCGTCAACCAGATGGACAAGTTCGGTCTGCTCCTCG 1840

Qy    926 AGGTTGGCAACGAGGGCATCGTGCTGCTGAAGAACGAGAACAACGTTCTGCCCTTGAGCA 985
Db   1841 CGACTCCGGCGCCCCGCCCCGAGCGTGACAAGGCGGGCGCCCAGGCGGTGTCCCGCAAGG 1900

Qy    986 AGAAGAAGAAGACGCTGATTGTCGGCCCCAACGCCAAGCAGGCCACATACCACGGCGGAG 1045
Db   1901 TCGCCGAGAACGGCGCGGTGCTCCTGCGCAACGAGGGCCAGGCCCTGCCGCTCGCCGGTG 1960

Qy   1046 GCTCTGCCGCACTCAGGGCCTACTACGCAGTCACTCCCTTTGACGGCCTCAGCAAGCAGC 1105
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Qy   1106 TCGAGACGCCGCCATCGTACACCGTCGGCGCCTACACCACCGTTCCTCCCATTCTAGGCG 1165
Db   2020 CTGGGCAGCGCCCACGTCGTCCCGGACTCGGCGGCGGCGCCGCTCGACACCATCAAGGCC 2079

Qy   1166 AGCAGTGCCTCACGCCCGACGGCGCTCCGGGCATGCGCTGGAGGGTCTTCAACGAGCCCC 1225
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Qy   1226 CTGGTACCCCTAACCGCCAGCACATTGACGAGCTCTTCTTCACCAAGACGGACATGCACC 1285
Db   2140 ATCCCGGCGGCGCAGCTCAGC------------------------CCGGCGTTCAACC 2173

Qy   1286 TGGTGGACTACTACCACCCCAAGGCGGCAGACACGTGGTACGCCGACATGGAGGGCACGT 1345
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Qy   1346 ACACCGCCGACGAGGACTGCACCTACGAGCTCGGCCTCGTCGTCTGCGGCACGGCAAAGG 1405
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Db   2234 CCGCCGACGGCGAGTACCGCATCTCGGTCAAGGCCACCGGTGGCTACGCGACGGTGCAG- 2292

Qy   1406 CGTACGTAGACGACCAGCTCGTCGTCGACAACGCCACCAAGCAGGTCCCCGGCGATGCCT 1465
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Db   2293 ----------------------------------------------CTCGGCAGCCACA 2305

Qy   1466 TCTTCGGCTCCGCCACCCGCGAGGAGACGGGCCGCATCAATCTCGTCAAGGGCAACACGT 1525
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Qy   1526 ACAAGTTCAAGATCGAGTTCGGCTCCGCACCCACCTACACCCTCAAGGGCGACACCATCG 1585
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Qy   1586 TCCCCGGCCACGGCTCCCTCCGCGTCGGCGGCTGCAAGGTCATTGACGACCAGGCCGAAA 1645
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Qy   1646 TCGAAAAGTCCGTCGCCCTCGCCAAGGAGCACGACCAGGTCATCATCTGCGCGGGCCTTA 1705
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Qy   1706 ACGCCGACTGGGAGACCGAGGGCGCCGACCGCGCGAGCATGAAGCTCCCCGGCGTGCTGG 1765
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Db   2515 --TACGACGACGGCACCGAGGGCGTCGACCGTCCGAACCTGTCGCTGCCGGGTACGCAGG 2572

Qy   1766 ACCAGCTCATTGCCGACGTGGCCGCCGCGAACCCAAACACCGTCGTCGTCATGCAGACGG 1825
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Db   2573 ACAAGCTGATCTCGGCGGTCGCCGACGCGAACCCGAACACGATCGTGGTCCTCAACACCG 2632

Qy   1826 GCACCCCCGAGGAGATGCCCTGGCTCGACGCCACGCCCGCCGTCATCCAGGCCTGGTACG 1885
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Db   2633 GTTCGTCGGTGCTGATGCCGTGGCTGTCCAAGACCCGCGCGGTCCTGGACATGTGGTACC 2692

Qy   1886 GCGGCAACGAGACGGGCAACTCCATTGCCGACGTCGTCTTTGGCGACTACAACCCCTCGG 1945
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Qy   1946 GCAAGCTGTCCCTCAGCTTCC------CCAAGCGCCTGCAGGACAACCCCGCGTTTCTCA 1999
          |||||||  | |  |||||||      || ||  || ||| | |  | |||     |  |
Db   2753 GCAAGCTCACGCAGAGCTTCCCGGCCGCCGAGAACCAGCACGCCGTCGCCGGCGACCCGA 2812

Qy   2000 ACTTCCGCACCGAGGCCGGGCGCACGCT---GTACGGCGAGGACGTCTACGTCGGGTACA 2056
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Db   2813 ACCGCTACCCGGGCGTCGACAACCAGCAGACGTACAGCGAGGGCATCCACGTCGGGTACC 2872

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RESULT 14
AF521878
LOCUS       AF521878               17665 bp    DNA     linear   BCT 29-JUL-2002
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DEFINITION  Streptomyces narbonensis desosamine biosynthetic gene cluster,
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ACCESSION   AF521878
VERSION     AF521878.1  GI:22001230
KEYWORDS    .
SOURCE      Streptomyces narbonensis.
  ORGANISM  Streptomyces narbonensis
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE   1  (bases 1 to 17665)
  AUTHORS   Bate,N. and Cundliffe,E.
  TITLE     The desosamine biosynthetic cluster of Streptomyces narbonensis,
            producer of narbomycin
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 17665)
  AUTHORS   Bate,N. and Cundliffe,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUN-2002) Biochemistry, Leicester University,
            University Road, Leicester LE1 7RH, UK
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Qy    206 CGCTCGGTTCCACATTCAACCAAACTCTGCTCGAAGAGGCAGGTAAGATGATGGCGCAAAG 265
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Db   5410 CACACGGCGGCCGGAACTACGAGACCTTCAGCGAGGACCCCCTGGTCTCCTCGCGCACCG 5469

Qy    386 CTGCGGCTCTCATCCGCGGCATTCAGAGCACTGGAGTGCAGGCTACGATCAAGCACTTTT 445
          | |  || |  |||   ||||| ||| |  | ||  ||  | | |||  |||||||||
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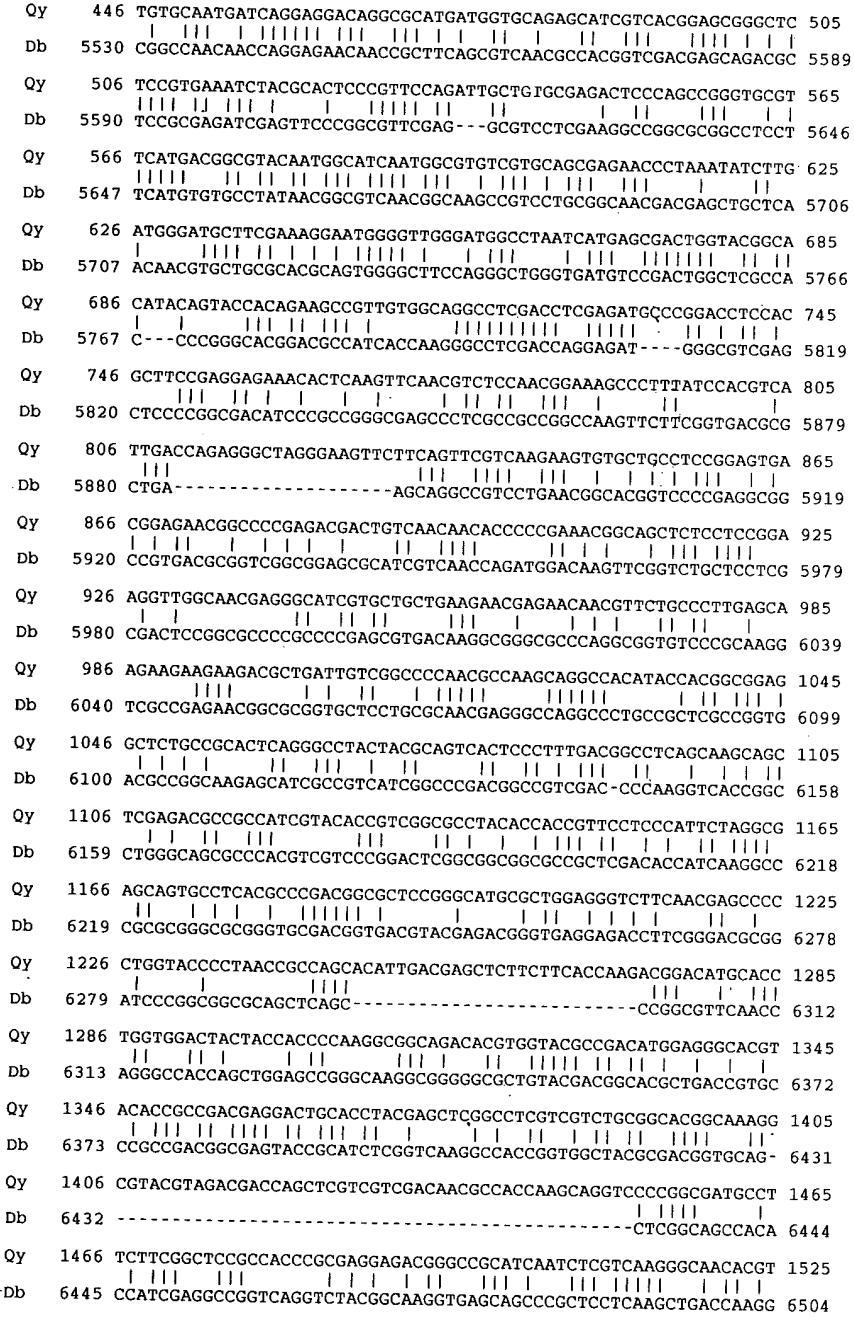

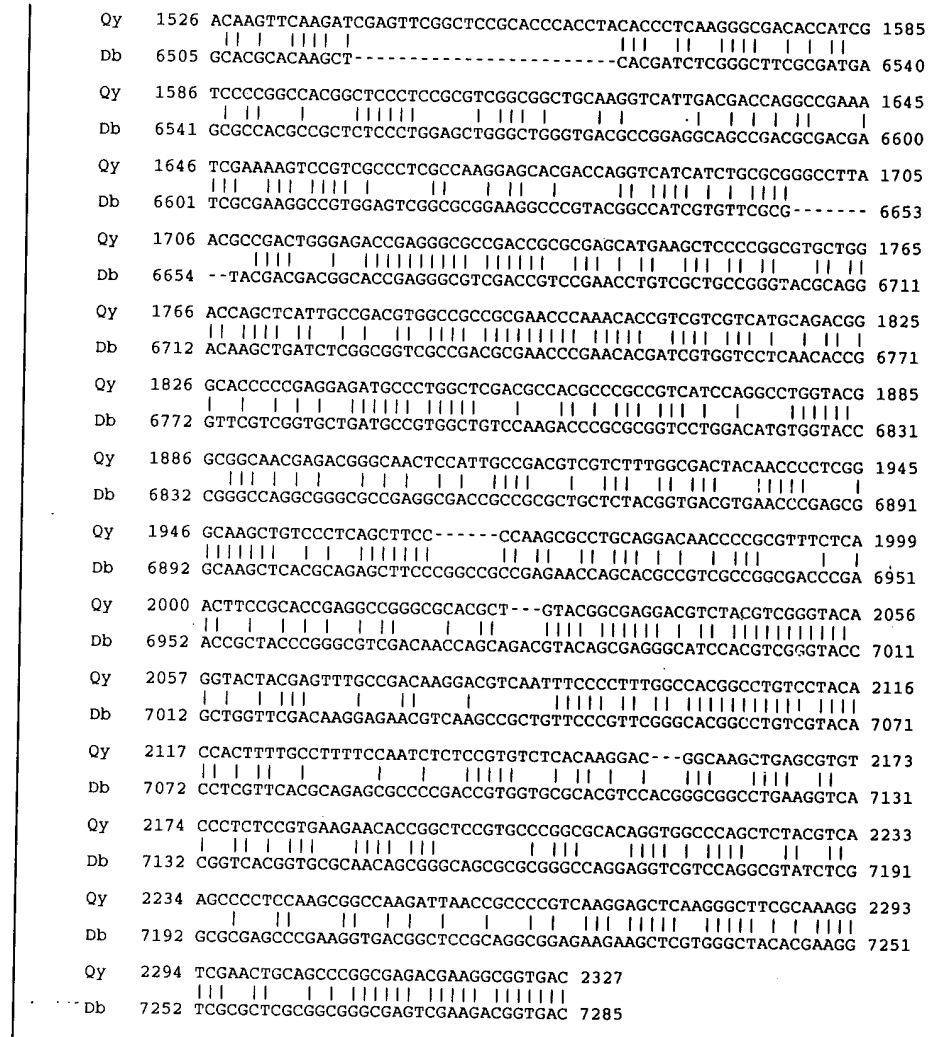

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DEFINITION Saccharopolyspora erythraea partial ermE and eryBIII genes and eryB gene.
ACCESSION Y14327
VERSION Y14327.1 GI:2982610
KEYWORDS beta-glucosidase; eryBI gene; eryBIII gene.
SOURCE Saccharopolyspora erythraea.
ORGANISM Saccharopolyspora erythraea
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Saccharopolyspora.
REFERENCE 1 (bases 1 to 2760)
AUTHORS Gaisser,S., Bohm,G.A., Doumith,M., Raynal,M.C., Dhillon,N., Cortes,J. and Leadlay,P.F.

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  TITLE     Analysis of eryBI, eryBIII and eryBVII from the erythromycin
            biosynthetic gene cluster in Saccharopolyspora erythraea
  JOURNAL   Mol. Gen. Genet. 258 (1-2), 78-88 (1998)
  MEDLINE   98273631
   PUBMED   9613575
REFERENCE   2  (bases 1 to 2760)
  AUTHORS   Leadlay,P.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUL-1997) P.F. Leadlay, Department Of Biochemistry,
            University Of Cambridge, Tennis Court Road, Cambridge CB2 1QW, UK
  REMARK    Updated by [3]
REFERENCE   3  (bases 1 to 2760)
  AUTHORS   Leadlay,P.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAR-1998) P.F. Leadlay, Department Of Biochemistry,
            University Of Cambridge, Tennis Court Road, Cambridge CB2 1QW, UK
COMMENT     On Mar 25, 1998 this sequence version replaced gi:2765397.
            Overlapping sequences: X60379, M11200.
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Qy   1711 GACTGGGAGACCGAGGGCGCCGACCGCGCGAGCATGAAGCTCCCCGGCGTGCTGGACCAG 1770
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Qy   1771 CTCATTGCCGACGTGGCCGCCGCGAACCCAAACACCGTCGTCGTCATGCAGACGGGCACC 1830
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Qy   2002 TTCCGCACCGAGGCCGGGCGCACGCTGTACGGCGAGGACGTCTACGTCGGGTACAGGTAC 2061
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Qy   2242 CAAGCGGCCAAGATTAACCGCCCCGTCAAGGAGCTCAAGGGCTTCGCAAAGGTCGAACTG 2301
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Db    261 GCACCGGGCGAGACCAAGCGCGTCCGGGTGCACGTCGCGGAGCGGGCCCTC 211
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Search completed: May 4, 2003, 03:05:15
Job time : 4797.77 secs